

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:14:48 ; Search time 9 Seconds
(without alignments)
502.864 Million cell updates/sec

Title: US-10-782-141-3

Perfect score: 3556

Sequence: 1 MNMMSYQNTNEYILDGSP.....CEGVQSLETKKEIVNSLFIN 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51463 seqs, 6734788 residues

Total number of hits satisfying chosen parameters: 51463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:

- 1: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pbp.*
- 2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pbp.*
- 3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pbp.*
- 4: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pbp.*
- 5: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pbp.*
- 6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pbp.*
- 7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pbp.*
- 8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	776.5	21.8	1210	7	US-11-058-727-4
2	776.5	21.8	1210	7	US-11-108-389-4
3	754.5	21.2	1206	7	US-11-058-727-2
4	754.5	21.2	1206	7	US-11-108-389-2
5	752	21.1	673	7	US-11-058-727-14
6	752	21.1	673	7	US-11-108-389-14
7	730	20.5	669	7	US-11-058-727-6
8	730	20.5	669	7	US-11-058-727-12
9	730	20.5	669	7	US-11-108-389-6
10	730	20.5	669	7	US-11-108-389-12
11	726	20.4	673	7	US-11-058-727-34
12	726	20.4	673	7	US-11-058-727-70
13	726	20.4	673	7	US-11-108-389-34
14	726	20.4	673	7	US-11-108-389-70
15	725	20.4	675	7	US-11-058-727-48
16	725	20.4	675	7	US-11-058-727-80
17	725	20.4	675	7	US-11-108-389-48
18	725	20.4	675	7	US-11-108-389-80
19	724.5	20.4	674	7	US-11-058-727-50
20	724.5	20.4	674	7	US-11-058-727-82
21	724.5	20.4	674	7	US-11-108-389-50
22	724.5	20.4	674	7	US-11-108-389-82
23	724	20.4	673	7	US-11-058-727-22
24	724	20.4	673	7	US-11-058-727-30
25	724	20.4	673	7	US-11-058-727-58

26	724	20.4	673	7	US-11-058-727-64	Sequence 64, Appl
27	724	20.4	673	7	US-11-058-727-66	Sequence 66, Appl
28	724	20.4	673	7	US-11-058-727-68	Sequence 68, Appl
29	724	20.4	673	7	US-11-058-727-90	Sequence 90, Appl
30	724	20.4	673	7	US-11-108-389-22	Sequence 22, Appl
31	724	20.4	673	7	US-11-108-389-30	Sequence 30, Appl
32	724	20.4	673	7	US-11-108-389-58	Sequence 58, Appl
33	724	20.4	673	7	US-11-108-389-64	Sequence 64, Appl
34	724	20.4	673	7	US-11-108-389-66	Sequence 66, Appl
35	724	20.4	673	7	US-11-108-389-68	Sequence 68, Appl
36	724	20.4	673	7	US-11-108-389-90	Sequence 90, Appl
37	723.5	20.3	674	7	US-11-058-727-44	Sequence 44, Appl
38	723.5	20.3	674	7	US-11-058-727-76	Sequence 76, Appl
39	723.5	20.3	674	7	US-11-108-389-44	Sequence 44, Appl
40	723.5	20.3	674	7	US-11-108-389-76	Sequence 76, Appl
41	723	20.3	673	7	US-11-058-727-8	Sequence 8, Appl
42	723	20.3	673	7	US-11-058-727-26	Sequence 26, Appl
43	723	20.3	673	7	US-11-108-389-8	Sequence 8, Appl
44	723	20.3	673	7	US-11-108-389-26	Sequence 26, Appl
45	723	20.3	675	7	US-11-058-727-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1

US-11-058-727-4

; Sequence 4, Application US/11058727

; Publication No. US20050261483A1

; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad

; APPLICANT: Ronald D. Flannagan

; APPLICANT: Rafael Herrmann

; APPLICANT: Theodore W. Kahn

; APPLICANT: Albert L. Lu

; APPLICANT: Billy Fred McCutchen

; APPLICANT: James K. Preenail

; APPLICANT: James F.H. Wong

; APPLICANT: Cao-Guo Yu

; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

; FILE OF INVENTION: Activity

; FILE REFERENCE: 35718/287809

; CURRENT APPLICATION NUMBER: US/11/058,727

; CURRENT FILING DATE: 2005-02-15

; PRIOR APPLICATION NUMBER: 60/391,786

; PRIOR FILING DATE: 2002-06-26

; PRIOR APPLICATION NUMBER: 60/460,787

; PRIOR FILING DATE: 2003-04-04

; PRIOR APPLICATION NUMBER: 10/606,320

; PRIOR FILING DATE: 2003-06-25

; NUMBER OF SEQ ID NOS: 134

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 1210

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-11-058-727-4

Query Match 21.8%; Score 776.5; DB 7; Length 1210;

Best Local Similarity 30.4%; Pred. No. 9.7e-58;

Matches 222; Conservative 130; Mismatches 272; Indels 107; Gaps 28;

QY 6 SYQNTNEYILDGSPNN--TNMSNRYPPAKDPNIFPINLD-----ACQGRP- 49

Db 2 SPNNQNEYIIDATPTSVNSNDSNRYPPAFNEPTNALQNMDYKDYLKMSAGNASEVPGSPSE 61

QY 50 ----WQDTWESVSDIVTIGTYLQFLLEPGIGIPVIFS-IINKLIPSSQGSVAALSICD 104

Db 62 VLVSGDAAKAAIDIV---GKLLSGLGVPPVPGVIVSLYTLQIDLTPSPGQKSQWEIFMEQ 118

QY 105 LVSIIRKEVDESVLSDGVADFEGEMTAYQDYLYHLEDWLTDSNPKKLADVVKQFQARE 164

Db 119 VEELINQKTAETAYARNKALSELEGLGNYYQ-LYLTALEEWNKENPNSGRALDVRNRFLD 177

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QY 165 EDFTKLAGSLSRQKAEIILLPTTYQANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTD 224
Db 178 SLFTQIMP-SFRVTNFEVFPFLVTYTOAANLHLLLDKASIFGEBWGM-----STTT 227
QY 225 CNERLKAKIK---EYNTYCVGWYKGLDQIROAGTSAEYVSKFNKFRREMTLAVLDIAI 281
Db 228 INNYDRQMKLTAEYSDHCWKYETGLAKL--GTSAKQWVDYNQFRREMTLTVLDVAL 285
QY 282 PPTYDFEKYPLATSVELTREIYTDVPG-----YSGNGYGMERFSPNSVEANGTRGGLVT 337
Db 286 FPNYDTRTYPMETKAQLTREVTDPGLAVNVSSIGSW-YDKAPSGFVIESSVIRPPHVD 344
QY 338 WLQADIDYSHSINLQIG-YLSGWGGTRHYEDFTK--GNGAFORMSGTTSN--NPRNIIFG 392
Db 345 YITGLTVTYQSRSSISARYIRHWAG--HQISYHRIFSDNIIKQMYGTNQLHSTSTFTD 402
QY 393 NTDIFKIISLARYAQ-PFVGYSIPRHLVSRAEFPTTLTNTFLYEVNSS---GYSTIE 447
Db 403 NYDIYKTLSDKAVLDIVFPGYTYIFFGMPVEFF-----MVNQLNTRKTLKYNPVS 456
QY 448 SVLPQINK---DLPPSRT-----NYSHRLSNAACVQ---NETSRVNVFGWTHSMKKDN 495
Db 457 DIIAGTRDSELELPETSDQPNYESYSHRLCHITSIPATGSTTGLVPVFSWTHRSADLIN 516
QY 496 RIYPDKITQIPAVKAFAL-PAGTGAGGVYTAGPGYTGDDVVTLPYQASL--KIRLTSAP 552
Db 517 AVHSDKITQIPVVKVSDLAPSTGPNNTVWSGPGFTGGGIIKVIKIRNGVVIISHMRVKISD 576
QY 553 TNKNYRVLRYASGGPGPFRVERWSPS-----SVSNANFSRPATGGYSSFDVVD----- 601
Db 577 INKEYSMRIRYASANTTEFYI---NPSEENVKSHAKTWNRGALTYNKFNTATLPPIKF 633
QY 602 TLVTTFNQSGVEIIIIQNLSGYHLIVDKVEFIPIDIQIEKCTKCFEGDICRCGVQSLET 661
Db 634 TTTEPFITLGAIFEAEDFLGIEAYIDRIEFIPVDETY-----EAEQDLEA 678
QY 662 KKEIVNSLFIN 672
Db 679 AKKAVNALFTN 689

```

RESULT 2

```

US-11-108-389-4
; Sequence 4, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis

```

US-11-108-389-4

```

Query Match 21.8%; Score 776.5; DB 7; Length 1210;
Best Local Similarity 30.4%; Pred. No. 9.7e-58;
Matches 222; Conservative 130; Mismatches 272; Indels 107; Gaps 28;
QY 6 SYQNTNEYEILDGSPNN--TNMSNRYPPFAKDNPFIINLD-----ACQGRP- 49
Db 2 SPNNQNEYEIIIDATFSTSVSNDNSNRYPPFANETNALQNMDYDKYLKMSAGNASSEYPSPE 61
QY 50 ----WQDTWESVSDIVTIGTYILQFLLEPGIGIPIVIFS-IINKLIPSSQSQSVAALSICD 104
Db 62 VLVSQDAAKAIDIV---GKLLSGLGVFPVGPVIVSLYQLIDILWPSGQKSQWEIFMEQ 118
QY 105 LVSIIRKEVDESIVSGVADFEGETAYQDYLYHLYEDMLTDSKNPKKLADVVKQFOARE 164
Db 119 VEELINQKIAEYARNKALSEGLGNVNY-LYLTAALEEWKENPNSRALRDVNRPFELD 177
QY 165 EDFTKLAGSLSRQKAEIILLPTTYQANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTD 224
Db 178 SLFTQIMP-SFRVTNFEVFPFLVTYTOAANLHLLLDKASIFGEBWGM-----STTT 227
QY 225 CNERLKAKIK---EYNTYCVGWYKGLDQIROAGTSAEYVSKFNKFRREMTLAVLDIAI 281
Db 228 INNYDRQMKLTAEYSDHCWKYETGLAKL--GTSAKQWVDYNQFRREMTLTVLDVAL 285
QY 282 PPTYDFEKYPLATSVELTREIYTDVPG-----YSGNGYGMERFSPNSVEANGTRGGLVT 337
Db 286 FPNYDTRTYPMETKAQLTREVTDPGLAVNVSSIGSW-YDKAPSGFVIESSVIRPPHVD 344
QY 338 WLQADIDYSHSINLQIG-YLSGWGGTRHYEDFTK--GNGAFORMSGTTSN--NPRNIIFG 392
Db 345 YITGLTVTYQSRSSISARYIRHWAG--HQISYHRIFSDNIIKQMYGTNQLHSTSTFTD 402
QY 393 NTDIFKIISLARYAQ-PFVGYSIPRHLVSRAEFPTTLTNTFLYEVNSS---GYSTIE 447
Db 403 NYDIYKTLSDKAVLDIVFPGYTYIFFGMPVEFF-----MVNQLNTRKTLKYNPVS 456
QY 448 SVLPQINK---DLPPSRT-----NYSHRLSNAACVQ---NETSRVNVFGWTHSMKKDN 495
Db 457 DIIAGTRDSELELPETSDQPNYESYSHRLCHITSIPATGSTTGLVPVFSWTHRSADLIN 516
QY 496 RIYPDKITQIPAVKAFAL-PAGTGAGGVYTAGPGYTGDDVVTLPYQASL--KIRLTSAP 552
Db 517 AVHSDKITQIPVVKVSDLAPSTGPNNTVWSGPGFTGGGIIKVIKIRNGVVIISHMRVKISD 576
QY 553 TNKNYRVLRYASGGPGPFRVERWSPS-----SVSNANFSRPATGGYSSFDVVD----- 601
Db 577 INKEYSMRIRYASANTTEFYI---NPSEENVKSHAKTWNRGALTYNKFNTATLPPIKF 633
QY 602 TLVTTFNQSGVEIIIIQNLSGYHLIVDKVEFIPIDIQIEKCTKCFEGDICRCGVQSLET 661
Db 634 TTTEPFITLGAIFEAEDFLGIEAYIDRIEFIPVDETY-----EAEQDLEA 678
QY 662 KKEIVNSLFIN 672
Db 679 AKKAVNALFTN 689

```

RESULT 3

```

US-11-058-727-2
; Sequence 2, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu

```

```
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-058-727-2

Query Match      21.2%; Score 754.5; DB 7; Length 1206;
Best Local Similarity 31.4%; Pred. No. 7.1e-56;
Matches 233; Conservative 119; Mismatches 258; Indels 131; Gaps 32;

QY      6 SYQNTNEYILDGSPNN--TNMSNRYPPFAKDPNIPFNL-----ACQGRP- 49
Db      2 SPNNQNEYIIDATPSTSVSNDNSNRYPPFANEPTNALQNMDYKDYKMSAGNASEYPGSPE 61
QY      50 ----WQDTWESVDIVTIGTYILOFLEPGIGIPVIFS-IINKLIPSSGQSVAALSID 104
Db      62 VLVSQDAAKAAIDIV---GKLLSGLGVFPVGPVLSYLTQLDILWPSEKQWEIFMEQ 118
QY      105 LVSIIRKEVDESVLSDGVADFEGETAYQDYLYLHLEDWLTDSKNPKKLADVVKQFOARE 164
Db      119 VVELINQKIAEYARNKALSELGLGNYYQ-LYLTALKEEENPNRSRALRDVNRFEILD 177
QY      165 EDFTKLAGLSRQKAEILLPTTYQOANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTD 224
Db      178 SLFTQYMP-SPRVTFNFPVFLTYVYMAANLHLLKLDASIFGEWGW-----STTT 227
QY      225 CNERLKAKIK---EYTNVCVGNKGLDQIRQAGTSAEVSWSKFNKFRREMTLAVLDIAI 281
Db      228 INNYDROMKLTAEYSDHCVKWYETGLAKLK--GTSAKQWVDYVQFRRMTLAVLDVVAL 285
QY      282 PPTDYFEKYPLATSVELTREIYTDVPG---YSGGNYGWERFFSNVSVEANGTRGPGVLT 337
Db      286 FPNYDTRYPMETKAQLTREYVTDPLGAVNVSSIGSW-YDKAPSGFVIESVIRPPHVD 344
QY      338 WLQADIIYSHSINLQGL-YLSGWGGTR-HYEDFTKNGAFORMSGTTSN--NPRNIIFGN 393
Db      345 YITGLTVYTVQSRSSISSARYIRHWAGHOISYHRVSRGSN-LQOMYGTQNLHSTSTFDFTN 403
QY      394 TDFIKIISLARYAMO-PFVGYISIPRHLVSRABFF-----PTTLNTFLYE-VNSSGYSQTI 446
Db      404 YDIYKTLSDKAVLLDIVPGYTVYIFGMEPEVEFFVMVNLNTRKTLKYNPVSKDIIASTR 463
QY      447 ESVLPGINKOLPPSRT-----NYSRLSNAACVQ---NETSRVNVFGWTHTSMKKNRI 497
```

```
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-058-727-2

Query Match      21.2%; Score 754.5; DB 7; Length 1206;
Best Local Similarity 31.4%; Pred. No. 7.1e-56;
Matches 233; Conservative 119; Mismatches 258; Indels 131; Gaps 32;

QY      6 SYQNTNEYILDGSPNN--TNMSNRYPPFAKDPNIPFNL-----ACQGRP- 49
Db      2 SPNNQNEYIIDATPSTSVSNDNSNRYPPFANEPTNALQNMDYKDYKMSAGNASEYPGSPE 61
QY      50 ----WQDTWESVDIVTIGTYILOFLEPGIGIPVIFS-IINKLIPSSGQSVAALSID 104
Db      62 VLVSQDAAKAAIDIV---GKLLSGLGVFPVGPVLSYLTQLDILWPSEKQWEIFMEQ 118
QY      105 LVSIIRKEVDESVLSDGVADFEGETAYQDYLYLHLEDWLTDSKNPKKLADVVKQFOARE 164
Db      119 VVELINQKIAEYARNKALSELGLGNYYQ-LYLTALKEEENPNRSRALRDVNRFEILD 177
QY      165 EDFTKLAGLSRQKAEILLPTTYQOANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTD 224
Db      178 SLFTQYMP-SPRVTFNFPVFLTYVYMAANLHLLKLDASIFGEWGW-----STTT 227
QY      225 CNERLKAKIK---EYTNVCVGNKGLDQIRQAGTSAEVSWSKFNKFRREMTLAVLDIAI 281
Db      228 INNYDROMKLTAEYSDHCVKWYETGLAKLK--GTSAKQWVDYVQFRRMTLAVLDVVAL 285
QY      282 PPTDYFEKYPLATSVELTREIYTDVPG---YSGGNYGWERFFSNVSVEANGTRGPGVLT 337
Db      286 FPNYDTRYPMETKAQLTREYVTDPLGAVNVSSIGSW-YDKAPSGFVIESVIRPPHVD 344
QY      338 WLQADIIYSHSINLQGL-YLSGWGGTR-HYEDFTKNGAFORMSGTTSN--NPRNIIFGN 393
Db      345 YITGLTVYTVQSRSSISSARYIRHWAGHOISYHRVSRGSN-LQOMYGTQNLHSTSTFDFTN 403
QY      394 TDFIKIISLARYAMO-PFVGYISIPRHLVSRABFF-----PTTLNTFLYE-VNSSGYSQTI 446
Db      404 YDIYKTLSDKAVLLDIVPGYTVYIFGMEPEVEFFVMVNLNTRKTLKYNPVSKDIIASTR 463
QY      447 ESVLPGINKOLPPSRT-----NYSRLSNAACVQ---NETSRVNVFGWTHTSMKKNRI 497
Db      464 DSEL-----ELPPTSDQPNYESYSHRLCHITSIIPATGNTTGLVPVFSWTHRSADLNNTI 518
QY      498 YPDKITQIPAVKAF-ALPAGTYAGGYTAGPGYTGDDVV-----TLPYQASLKI 546
Db      519 YSDKITQIPAVKCNWNLFPV-----VYKGFHTGGDLLQYNRSTGSGVTU-FLARYGL 571
QY      547 RLTSAPTNNKYRLRYASGGPGPFVRVERWSPSSVSNANFSRATGG-----YSSFDVY 600
Db      572 ALEKA---GKYRVRLRYATDADVLH-----VNDQIQMPKTMNPGEDLTSKFKYA 620
QY      601 DTLVTTFNQSGVEIIQN-----LSGYHLIVDKVEFIFIDIQIEKCTKQCEGIDIC 651
Db      621 DAITTLNATDSSSLAKNGLBDPNSTLSGI-VYVDRIEFIVDETY-----666
QY      652 RCEGVQSLETKKEIVNSLFIN 672
```

Db 464 DSEL-----ELPETSDDPNYESYSHRLCHITSIPATGTTGLVPVFSWTHRSADLNWTI 518
Qy 498 YPDKITQIPAVKAF-ALPAGTGYAGGYTAGPGYTGDDVV-----TLPYQASLKI 546
Db 519 YSDKITQIPAVKWDNFPV-----VYKPGHTGGDLQYNRSTGSGVTL-FLARYGL 571
Qy 547 RLTSAPTWNVRLRYASGGPFRVERWSPSSVSNANFSPATGG-----YSSPDYV 600
Db 572 ALEKA---GKYRVLRYATDAIVLH-----VNDQAQIOMPKTMNFGEDITSKTFKVA 620
Qy 601 DTLVTTFNQSQVEIIION-----LSGVHLIVDKVEFIPIDIQIEKCTKQCEGDIC 651
Db 621 DAITTLNATUSSALKKNLGEDPNSTLSGI-VYVDRIEFIPVDETY-----666
Qy 652 RCEGVQSLETKKEIVNSLFIN 672
Db 667 --EAEQDLEAKKAVNALFTN 685

RESULT 5

US-11-058-727-14
; Sequence 14, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-11-058-727-14

Query Match 21.1%; Score 752; DB 7; Length 673;
Best Local Similarity 30.5%; Pred. No. 4.9e-56;
Matches 212; Conservative 128; Mismatches 262; Indels 92; Gaps 27;
Qy 6 SYQNTNEVEILDGSPNN--TNMSNRYPPAKDPNIPINLD-----ACQGRP- 49
Db 2 SPNNQNEVEIIDATPSTSVSNDNSNRYPPAFNEPTNALQNMDYKDYLKMSAGNASEYPGSP 61
Qy 50 ----WQDTWESVSDIVTIGTYILQFLLEPGIGIPVIFS-IINKLIPSSGQSVAAISICD 104
Db 62 VLVSQDAKAADIV---GKLLSLGVFPVGPVIVSLYTLQDLILWPSQKQWEIFMEQ 118
Qy 105 LVSIIRKEVDSVLSDGVADFGEMTAYQDYILHYLEDMLTDKSNPKLADVVVKQFAORE 164
Db 119 VEELINQKIAEYARNKALSEGLEGNQY-LYLTALEEWNKPNNGSRALRDVRNRFELD 177
Qy 165 EDFTKLLAGLSRQKAEILLTPTVQANVHLLLRDAVKYKKEGLVCPFLPYGSGRDT 224
Db 178 SLFTQYMP-SFRVTNFEVPFLTVYTQANLHLLLLKQASIFGEWGW-----STTT 227

Qy 225 CNERLKAKIK---EYTNVCVGHYNKGLDQIROAGTSAEVSXKFNKFRREMTLAVLDLIAI 281
Db 228 INNYDROKMLTAEYSDHCHVKWYETGLAKLK--GTSAKQWQVNDYNQFRREMTLTVLDVVAL 285
Qy 282 PFTYDFEYKPLATSEVELTREIYTDVPG-----YSGGNYGWERPFPSFNSVEANGTRGPGGLVT 337
Db 286 FPNYDTRIYPMETKAQLTREYVTDPLGAVNVSSISGSW-YDKAPSGVIESSVIRPHVPD 344
Qy 338 WLOADIYSHSINLOLG-YLSGWGTRHYVEDFTK--GNCAFORMSGTGN--NPRNIIFG 392
Db 345 YITGLTVVTQSRSSISSARYIRHWAG--HQISYHRIFSDNIILKQMYGTGNQLHSTSTFDEPT 402
Qy 393 NTFDIEKILSARYAMQ-PEVGYSIPIRHLVSRAREFPTTLTFLYEYVNS-----GYSQTIE 447
Db 403 NYDIYKTLSKDAVLIDIVPGYTIFFGMPVEVEFF-----MVNQNNTRKTLKYNPVSK 456
Qy 448 SVLPGINK---DLPPSRT-----NYSHRLSNAACVQ-----NETSRVNVFGWTHTSKKON 495
Db 457 DIIAGTRDSELELPETSDQPNYESYSHRLCHITSIPATGSTTGLVPVFSWTHRSADLIN 516
Qy 496 RIYPDKITQIPAVKAPAL-PAGTGYAGGYTAGPGYTGDDVTLVPYQASL--KIRLTSAP 552
Db 517 AVHSDKITQIPVVKVYSDLAPSIITGPNNTVWSGPGFTGGIIVIRNGVLIISHMRVKISD 576
Qy 553 TNKNYRVLRYASGCGPFRVERWSPS-----SVSNANFSRPATGYSYSDFYVD-----601
Db 577 INKEYSMRIRYASANNTEFYI---NPSEENVKSHAQKTMNREALTYNKFNATLPPIKF 633
Qy 602 TLVTTFNQSGVEIILQNLGSHLIVDKVEFIPID 635
Db 634 TTTEPFITLGAIFEAEDFLGIEAYIDRIEFIPVD 667

RESULT 6

US-11-108-389-14
; Sequence 14, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-11-108-389-14

Query Match 21.1%; Score 752; DB 7; Length 673;
Best Local Similarity 30.5%; Pred. No. 4.9e-56;
Matches 212; Conservative 128; Mismatches 262; Indels 92; Gaps 27;
Qy 6 SYQNTNEVEILDGSPNN--TNMSNRYPPAKDPNIPINLD-----ACQGRP- 49
Db 2 SPNNQNEVEIIDATPSTSVSNDNSNRYPPAFNEPTNALQNMDYKDYLKMSAGNASEYPGSP 61

APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 669
TYPE: PRT
ORGANISM: Bacillus thuringiensis (truncated)
US-11-058-727-12

Query Match 20.5%; Score 730; DB 7; Length 669;
Best Local Similarity 31.7%; Pred. No. 3.5e-54;
Matches 223; Conservative 117; Mismatches 248; Indels 116; Gaps 31;
QY 6 SYONTNEYELDGSNN--TMSNRYPPAKDNPFPINLD-----ACQGRP- 49
DB 2 SPNNQNEYEIIDATSTSVSNDNSNRYPPANETNALQNDYKDYKMSAGNASEYFGSPE 61
QY 50 ----WQDTWESVSDIVTIGTYLIQFLLEPGIGIPVIFS--IINKLIPSSGQSVAAALSICD 104
DB 62 VLVSGQDAAKAIDIV---GKLSGLGVFPVGPVLSLTQTLIDILWPSGKESQWEIFMEQ 118
QY 105 LVSIIRKEVDESVDGADFEGETAYQDYLYLHYLEDWLTDKSNPKKLADVVVKQFQARE 164
DB 119 VEELINQKIAEYARNKALSEGLEGNQYQ-LYLTALEEWEENPNGRALRDVNRFEILD 177
QY 165 EDFTKLAGSLRQKAEILLPTTYQAAVNHLLLRDAVKYKKEWGLVCPPLYPGSGRTD 224
DB 178 SLFTQYMP-SFRVTNFEVDFLTYYAANAHLHLLKDSIFGEWGW-----STTT 227
QY 225 CNERLKAKIK---EYTNVCVGNKGLDQIRQAGTSAEYVSKFNKFRREMTLAVLDIAI 281
DB 228 INNYDRQMKLTAEYSDHCWKYETGLAKLK--GTSAKQWVDYQFRREMTLAVLDVVAL 285
QY 282 PPTYDFEYKPLATSVELTREIYTDVPG-----YSGGNYGWERFFSNVEANGTRGPGGLVT 337
DB 286 FPNYDTRIYPMETKAQLTREVTYDPLGAVNVSSIGSW-YDKAPSGFVIESSVIRPPHVPD 344
QY 338 WLOAIDIVSHSINLQLG-YLSCWGGTR-HYEDFTKNGAFQMSGTTSN--NPRNIIFGN 393
DB 345 YITGLTVVTQSRISISSARIYRWAGHQISYHRVSRGNS-LQMYGTQNLHSTSTPFDFTN 403
QY 394 TDFIKIISLARVAMQ-PFVGYSIPRHLVSRAEFF-----PTTLNTFLYE-VNSSGYSQTI 446
DB 404 YDIYKTLSDKAVLLDIVPGYTYIPFGMEPEFFVMVQNLNTRKTLKYNPVSODIIASTR 463
QY 447 ESVLPKINKDLPPSRT-----NYSHRLSNAACVQ---NETSRVNVFGWTHTSKMDNRI 497
DB 464 DSEL-----ELPPEYSDQPNYESHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTI 518
QY 498 YPDKITQIPAVKAF-ALPAGTGYAGGYTAGPGYTGDDVV-----TLFPYQASLKI 546
DB 519 YSDKITQIPAVKCDNLPPVP-----VVKPGFHTGGDLLQYNRSYSGVTL-FLARYGL 571
QY 547 RLTSAPTQKYNVRLRYAGSGPGPFAVERWSYSSVSNANFSRPAATG-----YSSFDVY 600
DB 572 ALEKA---GKYRVRRLRYATDADIVLH-----VNDAQIQMPTKNPNCGEDLTSTKTKVA 620
QY 601 DPLVTFTFNQSVEIILION-----LSGYHLIVDKVEFIPID 635
DB 621 DAITTLINLATDSSLALKNLGDPNSTLSGI-VYVDRIEFIPVD 663

RESULT 9

US-11-108-389-6
Sequence 6, Application US/11108389
Publication No. US20050261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal Activity
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 669
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Maize optimized Cry1218-1
US-11-108-389-6

Query Match 20.5%; Score 730; DB 7; Length 669;
Best Local Similarity 31.7%; Pred. No. 3.5e-54;
Matches 223; Conservative 117; Mismatches 248; Indels 116; Gaps 31;
QY 6 SYONTNEYELDGSNN--TMSNRYPPAKDNPFPINLD-----ACQGRP- 49
DB 2 SPNNQNEYEIIDATSTSVSNDNSNRYPPANETNALQNDYKDYKMSAGNASEYFGSPE 61
QY 50 ----WQDTWESVSDIVTIGTYLIQFLLEPGIGIPVIFS--IINKLIPSSGQSVAAALSICD 104
DB 62 VLVSGQDAAKAIDIV---GKLSGLGVFPVGPVLSLTQTLIDILWPSGKESQWEIFMEQ 118
QY 105 LVSIIRKEVDESVDGADFEGETAYQDYLYLHYLEDWLTDKSNPKKLADVVVKQFQARE 164
DB 119 VEELINQKIAEYARNKALSEGLEGNQYQ-LYLTALEEWEENPNGRALRDVNRFEILD 177
QY 165 EDFTKLAGSLRQKAEILLPTTYQAAVNHLLLRDAVKYKKEWGLVCPPLYPGSGRTD 224
DB 178 SLFTQYMP-SFRVTNFEVDFLTYYAANAHLHLLKDSIFGEWGW-----STTT 227
QY 225 CNERLKAKIK---EYTNVCVGNKGLDQIRQAGTSAEYVSKFNKFRREMTLAVLDIAI 281
DB 228 INNYDRQMKLTAEYSDHCWKYETGLAKLK--GTSAKQWVDYQFRREMTLAVLDVVAL 285
QY 282 PPTYDFEYKPLATSVELTREIYTDVPG-----YSGGNYGWERFFSNVEANGTRGPGGLVT 337
DB 286 FPNYDTRIYPMETKAQLTREVTYDPLGAVNVSSIGSW-YDKAPSGFVIESSVIRPPHVPD 344
QY 338 WLOAIDIVSHSINLQLG-YLSCWGGTR-HYEDFTKNGAFQMSGTTSN--NPRNIIFGN 393
DB 345 YITGLTVVTQSRISISSARIYRWAGHQISYHRVSRGNS-LQMYGTQNLHSTSTPFDFTN 403
QY 394 TDFIKIISLARVAMQ-PFVGYSIPRHLVSRAEFF-----PTTLNTFLYE-VNSSGYSQTI 446
DB 404 YDIYKTLSDKAVLLDIVPGYTYIPFGMEPEFFVMVQNLNTRKTLKYNPVSODIIASTR 463
QY 447 ESVLPKINKDLPPSRT-----NYSHRLSNAACVQ---NETSRVNVFGWTHTSKMDNRI 497

Db 464 DSEL-----ELPETSQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTI 518
QY 498 YPDKITQIPAVKAF-ALPAGTGVAGGYVTAGPYTGDDVV-----TLPYQASLKI 546
Db 519 YSDKITQIPAVKCDNLFPVP-----VVKGPHTGGDLLQYNRSTGSGVTGL-FLARYGL 571
QY 547 RLTSAPTNNKRYRLRYASGGPGPFVRWSPSSVSNANFSRSPATGG-----YSSFDDV 600
Db 572 ALEKA---GKYRVLRYATDADIVLH-----VNDQIQMPKTNPGEDLTSKTFKVA 620
QY 601 DTLVTFNQSVEIIION-----LSGYHLIVDKVEIFIPID 635
Db 621 DAITTLNLTADSSALKHNLGDPNSTLSGI-VYVDRIEFIPVD 663

RESULT 10

US-11-108-389-12
; Sequence 12, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-11-108-389-12

Query Match 20.5%; Score 730; DB 7; Length 669;
Best Local Similarity 31.7%; Pred. No. 3.5e-54; Mismatches 248; Indels 116; Gaps 31;
Matches 223; Conservative 117;
QY 6 SYQNTNEVEILDGSPNN--TNMSNRYPPAKDNPFPINLD-----ACQGRP- 49
Db 2 SPNNQNEVEIIDATSTSVSNDNRYPPAFNEPTNALQNDYKDYLMKSNAGNASEYPGSPE 61
QY 50 ----WQDTWESVDIVTIGTYLIQFLPEGIGIPVIFS-IINKLIPSGQSVAAALSICD 104
Db 62 VLVSQDAAKAAIDIV---GKLLSGLGVFPVGPVLSVLYQLDILWPSEKGSQWEIFMEQ 118
QY 105 LVSIIRKEVDSVLSDGVADPFGEMTAYQDYIHLWLTDSKNPKKLADVVQFQARE 164
Db 119 VEELINQIAEYARNKALSELBGLGNQYQ-LYLTALKEEENPNPNSRALRDVNRNFEILD 177
QY 165 EDETKLAGLSRQKAEIILLPTYQAAVNHLLLDARVKKYKGLVCPPLYPGSGRTD 224
Db 178 SLFTYMP-SFRVTNFEVFLTVYMAANLHLLLDKASIFGEWGW-----STTT 227
QY 225 CNERLKAKIK---EYTNVCVGYNKGDLQIROAGTSAEYVWSKFNKFRREMTLAVLDIAI 281
Db 228 INNYDRQMKLTAEYSDHCWKWYETGLAKLK--GTSAKQWDYDYNQFRREMTLAVLDVVAL 285

QY 282 FPYDPEKYPPLATSVLTRYITDIPVG-----YGGNGYGWERFFSFNSVEANGTRGPGLV 337
Db 286 FPNYDRTYPMETKAQLTREVTYDPLGAVNVSSIGSW-YDKAPSGFVIESVIRPPHVPD 344
QY 338 WLQADIDYSHSINLQIG-YLSGNGGTR-HYEDFTKNGAFQPMSCGTTSN--NPRNIIFGN 393
Db 345 YITGLTVYVYQTSRISISSARYIRHWAGHQISYHRSVRSN-LQOMYGTNQNLHSTSTFDFTN 403
QY 394 TDFIKIISLARVAMQ-PFVGYSIPRHLVSRAEFP-----PTLNTFLYE-VNSSGYSOTI 446
Db 404 YDIKYTLSDKADVLLDIVPGYTYIFPGMPEVEFPMVQNLNTRKTLKYNPVSKDIIASTR 463
QY 447 ESVLPGINKDLPSRT-----NYSRLSNAACVQ----NETSRVNVFGWTHSTMKKNRI 497
Db 464 DSEL-----ELPETSQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTI 518
QY 498 YPDKITQIPAVKAF-ALPAGTGVAGGYVTAGPYTGDDVV-----TLPYQASLKI 546
Db 519 YSDKITQIPAVKCDNLFPVP-----VVKGPHTGGDLLQYNRSTGSGVTGL-FLARYGL 571
QY 547 RLTSAPTNNKRYRLRYASGGPGPFVRWSPSSVSNANFSRSPATGG-----YSSFDDV 600
Db 572 ALEKA---GKYRVLRYATDADIVLH-----VNDQIQMPKTNPGEDLTSKTFKVA 620
QY 601 DTLVTFNQSVEIIION-----LSGYHLIVDKVEIFIPID 635
Db 621 DAITTLNLTADSSALKHNLGDPNSTLSGI-VYVDRIEFIPVD 663

RESULT 11

US-11-058-727-34
; Sequence 34, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-058-727-34

Query Match 20.4%; Score 726; DB 7; Length 673;
Best Local Similarity 31.6%; Pred. No. 7.8e-54;
Matches 225; Conservative 116; Mismatches 244; Indels 126; Gaps 33;
QY 6 SYQNTNEVEILDGSPNN--TNMSNRYPPAKDNPFPINLD-----ACQGRP- 49
Db 2 SPNNQNEVEIIDATSTSVSNDNRYPPAFNEPTNALQNDYKDYLMKSNAGNASEYPGSPE 61
QY 50 ----WQDTWESVDIVTIGTYLIQFLPEGIGIPVIFS-IINKLIPSGQSVAAALSICD 104
Db 62 VLVSQDAAKAAIDIV---GKLLSGLGVFPVGPVLSVLYQLDILWPSEKGSQWEIFMEQ 118


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; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-34

Query Match          20.4%; Score 726; DB 7; Length 673;
Best Local Similarity 31.6%; Pred. No. 7.8e-54;
Matches 225; Conservative 116; Mismatches 244; Indels 126; Gaps 33;

QY 6 SYQNTNEYILDGSPNN--TNMSNRYPPFAKDPNIFPINLD-----ACQGRP- 49
Db 2 SPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYLKMSAGNASEYFGSP 61
QY 50 ----WQDWESVSDIVTIGTYLIQFLLEPGIGIPVIFS-IINKLIPSSGQSVAALSICD 104
Db 62 VLVSGQDAKAAIDIV--GKLSGLGVFPVGPVLSYLTQIDILWPSEKQWEIFMEQ 118
QY 105 LVSIIRKEVDESVLSDGVADPFGEMTAYQDYLYHLEDWLTDSNP-----KKLADV 157
Db 119 VEELINQKIAEYARNKALSELEGLGNNYQ-LYLTALAEW---EENPNGRNGSRALRDVR 174
QY 158 KOFOAREEDFTKLLAGLSRQKAEIILLPTYVOAANVHLLLRDAVKYKKEWGLVCPPLY 217
Db 175 NRFEILDSLFTQMP-SFRVTNFEVPFLTVYMAANLHLLLLKDAISIFGEWGW----- 227
QY 218 PGSGRTDCNERLKAKIK---EYTNVCVGNKGLDQIROAGTSAEVSFKNFPRREMTLA 274
Db 228 ---STTTINYYDRQMKLTAEYSDHCWKYETGLAKL--GTSAKQWVDYNQFRREMTLA 282
QY 275 VLDIIAIFPTDYFEKYPLATSVELTREIYTDVPG-----YSGGNYGWERFFSNVSEANGT 330
Db 283 VLDVVALFPNYDTRTPMETKAQLTREVTYDPLGAVNVSSIGSW-YDKAPSGVIESVI 341
QY 331 RPPGLVTLWQADIDYSHSINLQAG-YLSCWGGTR-HYEDFTKNGAFQRMSTGTSN--NP 386
Db 342 RPPHVDYITGLTVYVTSQSSISSARYIRHWAGHQISYHRVSRGSN-LQQMYGTQNLHST 400
QY 387 RNIIFGNTDIFKIIISLARVAMQ-PFVGYSIPRHLVSRAEFF-----PTLTNTFLYE-VNS 439
Db 401 STFDFNTYDIYKTLSDKDAVLLDIVPGTYIFFGMEPEVEFFVFNQNLNTRKLYKNPVSK 460
QY 440 SGYSOTIESVLPGINKDLPPSR-----NYSHRLSNAACVQ---NETSRNVFGWTHTS 490
Db 461 DIIASTRDEL-----ELPETSDDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRS 515
QY 491 MKKDNRIYDPKTIQIPAVKAF-ALPAGTYAGYGTAGPGYTGDDV-----TLP 539
Db 516 ADLNTIYSDKITQIPAVKCDNLPFPV-----VVKFGHTGGDLLQYNRSTGVSGLT- 568
QY 540 YOASLKIRLTSAPTNNKVRVRYRYSAGGPGPFRVERWSPSSVSNANFSRATGG----- 593
Db 569 FLARYGLALEKA---GKRVRLRYATDADIVLH-----VNDQAIQMPKTNNGEDLT 617
QY 594 YSSFDYDVLVTFNQSGVEIIION-----LSGVHLIVDKVEFIPID 635
Db 618 SKTFKVAADAITVNLATDSSVAVKENVGDPNLSGI-VYVDRIEFIPVD 667
```

RESULT 14

```
US-11-108-389-70
; Sequence 70, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-70

Query Match          20.4%; Score 726; DB 7; Length 673;
Best Local Similarity 31.6%; Pred. No. 7.8e-54;
Matches 225; Conservative 116; Mismatches 244; Indels 126; Gaps 33;

QY 6 SYQNTNEYILDGSPNN--TNMSNRYPPFAKDPNIFPINLD-----ACQGRP- 49
Db 2 SPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYLKMSAGNASEYFGSP 61
QY 50 ----WQDWESVSDIVTIGTYLIQFLLEPGIGIPVIFS-IINKLIPSSGQSVAALSICD 104
Db 62 VLVSGQDAKAAIDIV--GKLSGLGVFPVGPVLSYLTQIDILWPSEKQWEIFMEQ 118
QY 105 LVSIIRKEVDESVLSDGVADPFGEMTAYQDYLYHLEDWLTDSNP-----KKLADV 157
Db 119 VEELINQKIAEYARNKALSELEGLGNNYQ-LYLTALAEW---EENPNGRNGSRALRDVR 174
QY 158 KOFOAREEDFTKLLAGLSRQKAEIILLPTYVOAANVHLLLRDAVKYKKEWGLVCPPLY 217
Db 175 NRFEILDSLFTQMP-SFRVTNFEVPFLTVYMAANLHLLLLKDAISIFGEWGW----- 227
QY 218 PGSGRTDCNERLKAKIK---EYTNVCVGNKGLDQIROAGTSAEVSFKNFPRREMTLA 274
Db 228 ---STTTINYYDRQMKLTAEYSDHCWKYETGLAKL--GTSAKQWVDYNQFRREMTLA 282
QY 275 VLDIIAIFPTDYFEKYPLATSVELTREIYTDVPG-----YSGGNYGWERFFSNVSEANGT 330
Db 283 VLDVVALFPNYDTRTPMETKAQLTREVTYDPLGAVNVSSIGSW-YDKAPSGVIESVI 341
QY 331 RPPGLVTLWQADIDYSHSINLQAG-YLSCWGGTR-HYEDFTKNGAFQRMSTGTSN--NP 386
Db 342 RPPHVDYITGLTVYVTSQSSISSARYIRHWAGHQISYHRVSRGSN-LQQMYGTQNLHST 400
QY 387 RNIIFGNTDIFKIIISLARVAMQ-PFVGYSIPRHLVSRAEFF-----PTLTNTFLYE-VNS 439
Db 401 STFDFNTYDIYKTLSDKDAVLLDIVPGTYIFFGMEPEVEFFVFNQNLNTRKLYKNPVSK 460
QY 440 SGYSOTIESVLPGINKDLPPSR-----NYSHRLSNAACVQ---NETSRNVFGWTHTS 490
Db 461 DIIASTRDEL-----ELPETSDDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRS 515
QY 491 MKKDNRIYDPKTIQIPAVKAF-ALPAGTYAGYGTAGPGYTGDDV-----TLP 539
Db 516 ADLNTIYSDKITQIPAVKCDNLPFPV-----VVKFGHTGGDLLQYNRSTGVSGLT- 568
QY 540 YOASLKIRLTSAPTNNKVRVRYRYSAGGPGPFRVERWSPSSVSNANFSRATGG----- 593
```

Db 569 FLARYGLALEKA---GKRVRLRYATDADIVLH-----VNDQAIQMPKTMNPGEDLT 617
 Qy 594 YSSFDYVDTLVTTFNQSGVEIIION-----LSGYHLIVDKVEFIPID 635
 Db 618 SKTFKVADAITTVNLATDSSVAVKHNKGEDPNSTLSGI-VYVDRIEFIPVD 667

RESULT 15

US-11-058-727-48
 ; Sequence 48, Application US/11058727
 ; Publication No. US20050261483A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andre R. Abad
 ; APPLICANT: Ronald D. Flannagan
 ; APPLICANT: Rafael Herrmann
 ; APPLICANT: Theodore W. Kahn
 ; APPLICANT: Albert L. Lu
 ; APPLICANT: Billy Fred McCutchen
 ; APPLICANT: James K. Presnail
 ; APPLICANT: James F.H. Wong
 ; APPLICANT: Cao-Guo Yu
 ; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
 ; FILE REFERENCE: 35718/287809
 ; CURRENT APPLICATION NUMBER: US/11/058,727
 ; CURRENT FILING DATE: 2005-02-15
 ; PRIOR APPLICATION NUMBER: 60/391,786
 ; PRIOR FILING DATE: 2002-06-26
 ; PRIOR APPLICATION NUMBER: 60/460,787
 ; PRIOR FILING DATE: 2003-04-04
 ; PRIOR APPLICATION NUMBER: 10/606,320
 ; PRIOR FILING DATE: 2003-06-25
 ; NUMBER OF SEQ ID NOS: 134
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 48
 ; LENGTH: 675
 ; TYPE: PRT
 ; ORGANISM: Bacillus thuringiensis (mutated)
 US-11-058-727-48

Query Match 20.4%; Score 725; DB 7; Length 675;
 Best Local Similarity 31.6%; Pred. No. 9.5e-54;
 Matches 225; Conservative 116; Mismatches 244; Indels 128; Gaps 33;
 Qy 6 SYQNTNEYIILDGSPNN--TNMSNRYPAKDPNIFPINLD-----ACQGRP- 49
 Db 2 SPNNQNEYIIDATPSTSVNSDSNRYPPANEPTNALQNDYKDYLKMSAGNASEYFGSPE 61
 Qy 50 ----WQDWESVDIVTIGTYLIQFLBPGIGGIPVPS-IINKLIPSSGQSVAAISICD 104
 Db 62 VLVSGQDAKAAIDIV--GKLLSLGLGVFPVGVISLVLTQLIDILWPSEKSGWEIFMEQ 118
 Qy 105 LVSIIRKEVDSVLSGDVADPEGEMTAYQDYLYHLYEDWLTOKSNP-----KCLAD 155
 Db 119 VEELINQIAEYARKAULEGLEGLGNQYQ-LYLTALEEW---EENPFRSGPNGSGRALRD 174
 Qy 156 VVKQFQAREEDFTKLLAGSLRSQKAEIILLPTTVQAAVNHLLLRDAVKYKKEWGLVCP 215
 Db 175 VVNREILDSLFTQYMP-SFRVTNEVFPPLTVYAAANLHLLLDKASIFGEWGW----229
 Qy 216 LYPGSGRTDCNRLKAKIK---EYTNVCGWYKGLDQIQOAGTSAEVMKFNKPRREMT 272
 Db 230 -----STTTINNYDROMKLTAEYSDHCWKWYETGLAKL--GTSAKQWVDYNQFREMT 282
 Qy 273 LAVLDIIALFPYDEKYPLATSVELTREIYTDVPG-----YSGGNYGWERFFSFNSVEAN 328
 Db 283 LAVLDVVALFPNYDTRTPMETKAQLTREYVTDPLGAVNVSSIGSW-YDKAPSFVGVISS 341
 Qy 329 GTRGPGVLTWQAIIDYSHSINLQLG-YLSGWWGGR-HYEDFTKNGAGFQMSGTTSN--384
 Db 342 VIRPHVFDYITGLVYVYTSRISISSARYIRHWAGHQISYHVRVSRGSN-LQQMYGTNQNLH 400

Search completed: December 15, 2005, 10:25:40
 Job time : 11 secs

Qy 385 NPRNIIFGNTDIFKIISLARYAMQ-PFVGYSIPIRHLVSRAEFF-----PTTLATFLYE-V 437
 Db 401 STSTFDFTNYDIYKTLSDAVLDDIVPGYTIYFFGMDPEVEFFPMVQNLNTRKTLKPNV 460
 Qy 438 NSSGYSQTIIESVLPKINKDLPFSRT-----NYSHRLSNAACVQ---NETSRVNVFGWTH 488
 Db 461 SKDIIASTRDSSEL-----ELPPETSQDPNYESYSHRLCHITSIPATGNTTGLVPVPSWTH 515
 Qy 489 TSMKKDNRIYPDKITQIPAVKAF-ALPAGTGYAGGVYTAGPGYTGDDV-----T 537
 Db 516 RSADLNNTIYSDKITQIPAVKCDNLPFVP-----VVRGPGHTGGDLLQYNRSTGSGVT 569
 Qy 538 LPYQASLKIRLTSAPTNNKRVRLRYASGCGPGFPRVERWSPSSVSNANFSRBPATGG---593
 Db 570 L-FLARYGLALEKA---GKRVRLRYATDADIVLH-----VNDQAIQMPKTMNPGED 617
 Qy 594 --YSSFDYVDTLVTTFNQSGVEIIION-----LSGYHLIVDKVEFIPID 635
 Db 618 LTSKTFKVADAITTVNLATDSSVAVKHNKGEDPNSTLSGI-VYVDRIEFIPVD 669

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2005, 09:53:11 ; Search time 48 Seconds
(without alignments)
1157.460 Million cell updates/sec

Title: US-10-782-141-3
Perfect score: 3556
Sequence: 1 MKNMNSYQNTNEYILDGSP.....CEGVQSLETKEIVNSLFIN 672

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/HCTUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	831	23.4	1242	2	US-09-001-982-12
2	831	23.4	1242	2	US-09-668-650-12
3	801.5	22.5	1156	2	US-09-001-982-10
4	801.5	22.5	1156	2	US-09-002-285-70
5	801.5	22.5	1156	2	US-09-589-477-70
6	801.5	22.5	1156	2	US-10-099-285A-70
7	801.5	22.5	1156	2	US-09-668-650-10
8	773	21.7	1157	1	US-07-876-280-30
9	773	21.7	1157	1	US-07-812-180A-2
10	773	21.7	1157	1	US-08-315-468-2
11	773	21.7	1157	2	US-07-941-650A-2
12	772.5	21.7	1229	1	US-08-100-709-4
13	772.5	21.7	1229	1	US-08-176-865-4
14	772.5	21.7	1229	1	US-08-474-038-4
15	772.5	21.7	1229	1	US-08-779-046-4
16	772.5	21.7	1229	1	US-08-881-340-4
17	770.5	21.7	802	2	US-09-661-322A-30
18	765	21.5	1167	2	US-10-089-678-1
19	754	21.2	1227	2	US-09-053-549-2
20	752.5	21.2	1149	1	US-07-915-203-2
21	752.5	21.2	1149	1	US-08-272-887-2
22	752.5	21.2	1149	1	US-08-789-449-2
23	746.5	21.0	1207	1	US-07-951-715A-7
24	746.5	21.0	1207	1	US-08-459-448A-7
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26	746.5	21.0	1207	2	US-08-459-504B-7
27	746.5	21.0	1207	2	US-08-459-444-7

28	746.5	21.0	1207	2	US-09-053-549-8	Sequence 8, Appli
29	746.5	21.0	1207	2	US-09-547-422-7	Sequence 7, Appli
30	746.5	21.0	1207	2	US-09-988-462-7	Sequence 7, Appli
31	733	20.6	1228	2	US-09-661-322A-38	Sequence 38, Appl
32	729	20.5	1169	1	US-08-315-468-4	Sequence 4, Appli
33	725.5	20.4	710	2	US-09-661-322A-42	Sequence 42, Appli
34	723.5	20.3	1227	1	US-08-448-170-8	Sequence 8, Appli
35	723.5	20.3	1227	2	US-08-961-803-9	Sequence 9, Appli
36	721.5	20.3	1227	2	US-09-661-322A-63	Sequence 63, Appl
37	718.5	20.2	1186	2	US-09-178-252-23	Sequence 23, Appl
38	718.5	20.2	1186	2	US-09-826-660-23	Sequence 23, Appl
39	716	20.1	719	2	US-08-286-870A-8	Sequence 8, Appli
40	715.5	20.1	648	2	US-08-286-870A-4	Sequence 4, Appli
41	707	19.9	643	2	US-09-178-252-25	Sequence 25, Appl
42	707	19.9	643	2	US-09-826-660-25	Sequence 25, Appl
43	689.5	19.4	1138	1	US-07-973-320-2	Sequence 2, Appli
44	689.5	19.4	1138	1	US-07-973-320-4	Sequence 4, Appli
45	688	19.3	652	2	US-08-996-441B-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-001-982-12
; Sequence 12, Application US/09001982
; Patent No. 6204246
; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J.
; APPLICANT: Stiekema, Willem J.
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6204246artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/602,737
; APPLICATION NUMBER: US 08/602,737
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-001-982-12

Query Match 23.4%; Score 831; DB 2; Length 1242;

Best Local Similarity 32.1%; Pred. No. 6.7e-70;

Matches 237; Conservative 128; Mismatches 246; Indels 128; Gaps 32;

QY 9 NTNEYILDGSPNTNMSN---RYPFKDPNIPINLDACQGRP---WQD-TWESVSDIV 61
DB 2 NQNKGIIL-GASNCGCSDDVAKYPLANNPYSALNLSNCSNLSINWNIIGDAKEAV 60

QY 62 TIGTYLIQLEPGIG-IPVIFSIINKLI-PSSGQVAALSTCDLVSIRKEVDESVL 119
Db 61 SIGTTIVSLITAPSTGLISIVYDLIGKVLGSSGQSIDLSICDLSIIDLRVSQSVLN 120
QY 120 DGVADFEGETAYQDYIYHLWDLTKSNPKLA--DVVKQFQAREEDFTKLL----- 171
Db 121 DGIADFNGLVLYRN-YLEALDSW---NKNPNSAAEELTRFRADSEFDRILTRGSLT 176
QY 172 -AGSLRQKAEILLPTVYQAAANVHLLLRDVAKYKFKFREMFLAVLDIIAIPPTDYFEKY 230
Db 177 NGGSLARQNAQIILLPSFASAAFFHLLLRDTRIGTNWG-----LYNATPFINYQSKLV 231
QY 231 AKIKETNYCVGWYKGLDQIRQAGTSARVSKFNKFRMFLAVLDIIAIPPTDYFEKY 290
Db 232 ELIELYDYCVHWYKNGFNLQRGTSATAWLEFHYRREMTLWLDIVASFSSLDITNY 291
QY 291 PLATSVELTREIYTDVGY-----SGNYGWERFF---SFNSVEANGTRGPGVLTWLOAID 343
Db 292 PIETDFQLSRVITYDPIGFVHRSSLRGESWFGVNNRANFSDLE-NAIPNPRPSWFLNNMI 350
QY 344 IYSHSINLQGLYSG-----WGTRHYEDFTKNGAF--ORMSGTTSNNPNIIFGNTDIF 397
Db 351 ISTGSLTLFVSPSTDRARVWYGSR--DRISPANSQFTELISQHTTATQTLGRN--IF 406
QY 398 KIISLARYAMQPFVGYSPRHLVSRABEFPPTT---LNTFLYE--VNSSGYS-----QTIES 448
Db 407 RVDSQACNLNDITYG-----VNRVAFYHDASEGSRQSVYEGYIRTTGIDNPRVQNT 459
QY 449 VLPNGKNDLPPSRNTVYSHLSNA-----ACVQNETSRVNVFGWTHSMKKNRIYD 500
Db 460 YLPGENS DI-PTPEDYTHLSNTINLTGLRQVANSRRSLVMYGTWKSLARNNTINPD 518
QY 501 KITQIPAVKAFALPAGTVAGGYTAGPGYTGDDVV---TLPYQASLKRLTASPTKNY 557
Db 519 RITQIPLVKGFRWGGTS-----VITGPGFTGDIILRRNTFGDFVSLQVINS-PITQRY 572
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Db 573 RLRFYASSRDARVILVTGAAGTVGCGQSVNPLQKTWEIGENLTSR-----TFRYT 625
QY 601 DTLVTTFNOSGVEII-----IQNLGYHLIVDKVEFIPIDIQIEKTKCQFEGDIC 651
Db 626 DFSNPFSPRANPDIIIGISQPLFGAGSISSGELYIDKIBIILADATFEA-----ESD-- 677
QY 652 RCEGVSQLETKKEIVNSLF 670
Db 678 -----LERAQKAVNALF 689

RESULT 2

US-09-668-650-12

Sequence 12, Application US/09668650

Patent No. 6780408

GENERAL INFORMATION:

APPLICANT: Bosch, Hendrick J.

TITLE OF INVENTION: Hybrid Toxin

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESS: No. 6780408artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA: #1.0, Version #1.30

APPLICATION NUMBER: US/09/668,650

FILING DATE: 22-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1242 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-668-650-12

Query Match 23.4%; Score 831; DB 2; Length 1242;

Best Local Similarity 32.1%; Pred. No. 6,7e-70;

Matches 237; Conservative 128; Mismatches 246; Indels 128; Gaps 32;

QY 9 NTNEYELDGSNNNTMSN---RYPPAKDPNIPFINDACQGRP---WOD-TWESVSDIV 61
Db 2 NQKHGII-GASCCGASDDVAKYPLANNPYSSALNLSNCSILNWINIIGDAAKEAV 60
QY 62 TIGTYLIQLEPGIG-IPVIFSIINKLI-PSSGQVAALSTCDLVSIRKEVDESVL 119
Db 61 SIGTTIVSLITAPSTGLISIVYDLIGKVLGSSGQSIDLSICDLSIIDLRVSQSVLN 120
QY 120 DGVADFEGETAYQDYIYHLWDLTKSNPKLA--DVVKQFQAREEDFTKLL----- 171
Db 121 DGIADFNGLVLYRN-YLEALDSW---NKNPNSAAEELTRFRADSEFDRILTRGSLT 176
QY 172 -AGSLRQKAEILLPTVYQAAANVHLLLRDVAKYKFKFREMFLAVLDIIAIPPTDYFEKY 230
Db 177 NGGSLARQNAQIILLPSFASAAFFHLLLRDTRIGTNWG-----LYNATPFINYQSKLV 231
QY 231 AKIKETNYCVGWYKGLDQIRQAGTSARVSKFNKFRMFLAVLDIIAIPPTDYFEKY 290
Db 232 ELIELYDYCVHWYKNGFNLQRGTSATAWLEFHYRREMTLWLDIVASFSSLDITNY 291
QY 291 PLATSVELTREIYTDVGY-----SGNYGWERFF---SFNSVEANGTRGPGVLTWLOAID 343
Db 292 PIETDFQLSRVITYDPIGFVHRSSLRGESWFGVNNRANFSDLE-NAIPNPRPSWFLNNMI 350
QY 344 IYSHSINLQGLYSG-----WGTRHYEDFTKNGAF--ORMSGTTSNNPNIIFGNTDIF 397
Db 351 ISTGSLTLFVSPSTDRARVWYGSR--DRISPANSQFTELISQHTTATQTLGRN--IF 406
QY 398 KIISLARYAMQPFVGYSPRHLVSRABEFPPTT---LNTFLYE--VNSSGYS-----QTIES 448
Db 407 RVDSQACNLNDITYG-----VNRVAFYHDASEGSRQSVYEGYIRTTGIDNPRVQNT 459
QY 449 VLPNGKNDLPPSRNTVYSHLSNA-----ACVQNETSRVNVFGWTHSMKKNRIYD 500
Db 460 YLPGENS DI-PTPEDYTHLSNTINLTGLRQVANSRRSLVMYGTWKSLARNNTINPD 518
QY 501 KITQIPAVKAFALPAGTVAGGYTAGPGYTGDDVV---TLPYQASLKRLTASPTKNY 557
Db 519 RITQIPLVKGFRWGGTS-----VITGPGFTGDIILRRNTFGDFVSLQVINS-PITQRY 572
QY 558 RVRLRYAS-----GGPGFPRVERMSVSSVSNANFSPRATGYSFDDY 600
Db 573 RLRFYASSRDARVILVTGAAGTVGCGQSVNPLQKTWEIGENLTSR-----TFRYT 625
QY 601 DTLVTTFNOSGVEII-----IQNLGYHLIVDKVEFIPIDIQIEKTKCQFEGDIC 651
Db 626 DFSNPFSPRANPDIIIGISQPLFGAGSISSGELYIDKIBIILADATFEA-----ESD-- 677
QY 652 RCEGVSQLETKKEIVNSLF 670
Db 678 -----LERAQKAVNALF 689

Db 626 DFSNPSFRANPDIIIGISEOPLGAGSISSELYIDKIEILLADATFEA-----ESD--- 677
QY 652 RCEGVOSLETKEIVNSLF 670
Db 678 -----LERAQKAVNALF 689

RESULT 3

US-09-001-982-10
; Sequence 10, Application US/09001982
; Patent No. 6204246

; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J.
; APPLICANT: Stiekema, Willem J.
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6204246artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/001,982
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1156 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-001-982-10

Query Match 22.5%; Score 801.5; DB 2; Length 1156;

Best Local Similarity 31.2%; Pred. No. 4e-67;

Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;

QY 9 NTEVEILDSGNNTNMSN--RYPEAKDPNIPFLNLDACQGRP---WOD-TWESVSDIV 61

Db 2 NQNKHGII--GASCCGASDDVAKYPLANNPYSSALNLSNCSIIINWINIIGDAKEAV 60

QY 62 TIGTYLIOPLBPGIGG-IPVIFSIINKLI-PSSQGSVAALSGICDLVSIIRKEVDSVL 119

Db 61 SIGTTIVSLITAPSLTGLISIVYDLIGKVLGSSGSGISDLSICDLISIIDLRVSQVLN 120

QY 120 DGVADEGEMTAYQDYLLHYLEDWLTDKSNPKLA--DVVKQFQAREEFTKLL----- 171

Db 121 DGIADFNGSVLLYRN--YLEALDSW---NKNPNSASAEELRTFRADSEFDRILTRGSLT 176

QY 172 -AGSLSRQAEILLPTTYQAAVNHLLARDVAKYKGLVCPPLYPGSGRTDCNERLK 230

Db 177 NGGSLARQNAQILLPSFASAFFHLLLRDLATRYGTNNG-----LYNATPFINYQSKLV 231

QY 231 AKIKEVTNYCVGYNKGLDQIRQAGTSAEWSKFNKFRMTLAVLDIIAIPPTDYFEKY 290

Db 232 ELIELYTYCVHWYNGFNELRQRTSATAWLEFHRYRREMLMWLDIVASFSSLDITNY 291

QY 291 PLATVELTREIYDVPVGY-----SGNGYWERFF---SFNSVEANGTRGPGLVTLWLQAD 343
Db 292 PIETDFOLSRVIVTDPIGFVHRSSLRGESWFSFVNANFSDLE-NAIPNRPSPWFLNNMI 350
QY 344 IYSHSINLQLGYLSG-----WGCTRHEDYFTKGNCAF--QRMSGTTNNPRHIIIGNTDIF 397
Db 351 ISTGSLTLPVSPSTDRARVWYGR--DRISPANSQFTELISGQHTTATQTILGRN--IF 406
QY 398 KIISLARYAMQPFVGYISIPRHLVSRAEFPPTT---LNTFLYE--VNSSGYS-----QTIES 448
Db 407 RVDSQACNLNDTYG-----VNRAVYHDAEGSORSVYEGVIRTGIDNPRVQNT 459
QY 449 VLPFGINKDLPPSRNTYSHRLSNA-----ACVQNETSRVNVFGWTHSTMKONRIYPD 500
Db 460 YLPGENS DI-PTPEDYTHILSTTINLTGGLRQVANSRRSSILVMYGTWTHKSLARNNTINPD 518
QY 501 KITQIPAVKAFALPAGTYAGGYVYAGPGVYTGDDVTLPYQASLKIRLTSAPTN--KNYR 558
Db 519 RITQIPLTKVDTTRGTGVSYN-----DPGFIGGALLQRTDHGSLGLVLRVQFPLHLRQOYR 573
QY 559 VRLRYASGGPGPFRVERWSPSSVSNANFSRPAT-----GCYSSFDYVDVTLVTTNQ 609
Db 574 IRVRYAS-----TTNIRLSVNGSFGTISQNLPSWTMLRGEDLRYGSFAIREFTSIRPTASP 629
QY 610 SGVEIIIQ-NLSGYHLIVDKVEPIPIDIQIEKTKCFEGDICEGVQSLETKKEIVNS 668
Db 630 DQIRLTIEPSFIRQEVYVDRIEFIPVN-----PTR-----EAKEDLEAAKAVAS 674
QY 669 LF 670
Db 675 LF 676

RESULT 4

US-09-002-285-70

; Sequence 70, Application US/09002285

; Patent No. 6369213

; GENERAL INFORMATION:

; APPLICANT: Schnepf, H. Ernest

; APPLICANT: Wicker, Carol

; APPLICANT: Narva, Kenneth E.

; APPLICANT: Walz, Michelle

; APPLICANT: Stockhoff, Brian

; APPLICANT: Muller-Cohn, Judy

; TITLE OF INVENTION: Toxins Active Against Peets

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: Florida

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/002,285

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/886,615

; FILING DATE: 1-JUL-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/674,002

; FILING DATE: 1-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Sanders, Jay M.

; REGISTRATION NUMBER: 39,355

; REFERENCE/DOCKET NUMBER: MA-701C2

```

GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Tokins Active Against Peats
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-589-477-70

Query Match      22.5%; Score 801.5; DB 2; Length 1156;
Best Local Similarity 31.2%; Pred. No. 4e-67;
Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31

Qy   9 NTNVEYILDGSPNNNTNSN---RYPPAKDPIFPILNDACQGRP---WQD-TWESVSDIV 61
Db   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
    2 NONKHGI-I-GASNCGCASDDVAKPYPLANNPYSSALNLNSCONSSLINWINIGDAAKEAV 60

Qy   62 TIGVLVQLFLPGIGG-IPVFISIIKLI-I-PSSQSQAALSIDCVLSIIRKEVDSEVLS 119
Db   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
    61 SIGTIVSLITAPSETGLISIVLDLIGLVGGSGGSISDSISICDLISIIDLRVSQSVLN 120

Qy   120 DGVAADPEGETAYQDYLYHLEDWLTDKSNPKCLA--DVVKQFOQAREEDFTKLL----- 171
Db   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
    121 DGIADFNGSVLLYRN-VLEALDSW--NKNPNASAEBELTRFRJADSEFDRILTRGSILT 176

Qy   172 -AGSLSRQKABILLPYTVQAAHVHLLLRRDAVYKKEWGLVCPPYPCSGRTDCNRUK 230
Db   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
    177 NGGSLARQNAQILLPSPFAAFPHLLLLRDATRYGTWNW-----LYNATPFINYQSKLV 231

Qy   231 AKIEKYTCVGVNWKGIDQIRQAGTSAEVSKENKPRMTLAVLDIIAIFPTVDFEY 290
Db   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
    232 ELISLYTDYCVVHWNRGFNEURQGTSTATALEFHRYREMTLMWLDIVASFSSLDITNY 291

Qy   291 PLATSVELTRIYPDVGYY-----SCGNYGWERFF----SFNSVEANGTRGPGLVTWLQAI 343

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Qy	291	PLATSVELTREIYDPVGY-----GGGNVGWRPF---SFNSVEANGTRGPGVLVWLQALD	343
Qy	232	ELIELYDYCVHWRNGFNELRQGTSAWLEFHYRYREMTLMVLDIVASPSLLDITNY	291
Db	231	AKLSLEINICVGNINAGLQQLKQASISHSVPSNATNFAREMLVADLVLLAFILDFENI	291
Qy	231	AKLSLEINICVGNINAGLQQLKQASISHSVPSNATNFAREMLVADLVLLAFILDFENI	291

Db 292 PIETDFQLSRVYITDPDGFVHRSSLRGESWFSVNRANFSDLE-NAIPNRPSPWFLNNMI 350
QY 344 IYSHSINLQGLVLSG-----WGGTRHYEDFTKGNF--ORMSGTTSNPNRIIFGNTDIF 397
Db 351 ISTGSLTLPVSPSTDRARVWYGR--DRISPANSQITELISQHTTATQTLGRN--IF 406
QY 398 KIISLARYAMQPFVGYSPRHLSVRAEFPTT---LNTFLYE--VNSSGYS-----QTIES 448
Db 407 RVDSQACNLNDTTYG-----VNRAVFYHDASEGSRQSVYEGYIRTTGIDNPRVQNT 459
QY 449 VLPKINKDLPSPRTNYSHLSNA-----ACVQNETSRVNVFGWTHSMKKDNRIYD 500
Db 460 YLPGENS DI-PTPEDYTHLSTTINLTGGLRQVASNRRSSLVNMGWTHKSLARNNTINPD 518
QY 501 KITQIPAVKAFALPAGTGVAGGVYTAGPGVGTGGDVVTLTPYQASLKRLTSAPT--KNYR 558
Db 519 RITQIPLTVDTRGTGVSYN-----DPGFIGALLQRTDGHSLGVLVQFPHLRQYR 573
QY 559 VRLRYASGGPGPRVVERVSPSSVSNANFSRPAT-----GGYSFDYVDTLVTTFNQ 609
Db 574 IRVRYAS-----TTNIRLSVNGSFGTISQNLPSMTMLGEDLRYGSFAIRENTSIRPTASP 629
QY 610 SGVEIIIQ-NLSGYHLIVDKVEFIPIDIQIEKCTKCFEGDICRCGVQSLETKEIVNS 668
Db 630 DQIRLTIEPSFIRQEVYVDRIEFIPV-----PTR-----EAKEDLEAAKAVAS 674
QY 669 LF 670
Db 675 LF 676

RESULT 6

US-10-099-285A-70
; Sequence 70, Application US/10099285A
; Patent No. 6752992

GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest

Wicker, Carol

Narva, Kenneth E.

Walz, Michelle

Stockhoff, Brian

Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Pests

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/099,285A

FILING DATE: 02-Jul-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/002,285

FILING DATE: 31-DEC-1997

APPLICATION NUMBER: US 08/886,615

FILING DATE: 1-JUL-1997

APPLICATION NUMBER: US 08/674,002

FILING DATE: 1-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-701C2D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-099-285A-70

Query Match 22.5%; Score 801.5; DB 2; Length 1156;
Best Local Similarity 31.2%; Pred. No. 4e-67;
Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;

QY 9 NITVEYILDGSPNNTWNSN---RYPFAKDNIPIINLDACQGRP---WQD-TWESVSDIV 61
Db 2 NQKHGII-GASNCGCASDDVAKYPLANNPYSSALNLSQNSILNWINIIGDAAKEAV 60
QY 62 TIGTYLIQFLLEPGIGG-IPVIFSIINKLI-PSGQSVAAISICDLVSIIRKEVDESVL 119
Db 61 SIGTTIVSLITAPSLTGLISIVYDLIGKVLGGSSGQSIDLSICDLSIIDLRVSQSVLN 120
QY 120 DGVADPEGEMTAYQDYLYLHYLEDWLTDKSNPKLA--DVVKQFOAREEDFTKLL----- 171
Db 121 DGIADPNGSVLLYRN-YLEALDSW---NKNPNSASAEELTRFRIADSEDFRILTRGSLT 176
QY 172 -AGSLSRQKAEIILLPTVYQAAVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNRLK 230
Db 177 NGGSLARQNAQIILLPSFASAAFFHLLLRDARTYGTNMG-----LYNATPFINYQSKLV 231
QY 231 AKIKEYTNCVGVWYKGLDQIRQAGTSAEWSKFNFRREMTLAVLDIIAIFPTDYDEKY 290
Db 232 ELIELYTDYCVHYNRGNFRELQRTGSATAWLEFHYRREMTLAVLDIVASFSLDITNY 291
QY 291 PLATSVELTREIYTDVPGY-----SGGNYGWREF--SFNSVEANGTRGGLVTLQAI 343
Db 292 PIETDFQLSRVYITDPDGFVHRSSLRGESWFSVNRANFSDLE-NAIPNRPSPWFLNNMI 350
QY 344 IYSHSINLQGLVLSG-----WGGTRHYEDFTKGNF--ORMSGTTSNPNRIIFGNTDIF 397
Db 351 ISTGSLTLPVSPSTDRARVWYGR--DRISPANSQITELISQHTTATQTLGRN--IF 406
QY 398 KIISLARYAMQPFVGYSPRHLSVRAEFPTT---LNTFLYE--VNSSGYS-----QTIES 448
Db 407 RVDSQACNLNDTTYG-----VNRAVFYHDASEGSRQSVYEGYIRTTGIDNPRVQNT 459
QY 449 VLPKINKDLPSPRTNYSHLSNA-----ACVQNETSRVNVFGWTHSMKKDNRIYD 500
Db 460 YLPGENS DI-PTPEDYTHLSTTINLTGGLRQVASNRRSSLVNMGWTHKSLARNNTINPD 518
QY 501 KITQIPAVKAFALPAGTGVAGGVYTAGPGVGTGGDVVTLTPYQASLKRLTSAPT--KNYR 558
Db 519 RITQIPLTVDTRGTGVSYN-----DPGFIGALLQRTDGHSLGVLVQFPHLRQYR 573
QY 559 VRLRYASGGPGPRVVERVSPSSVSNANFSRPAT-----GGYSFDYVDTLVTTFNQ 609
Db 574 IRVRYAS-----TTNIRLSVNGSFGTISQNLPSMTMLGEDLRYGSFAIRENTSIRPTASP 629
QY 610 SGVEIIIQ-NLSGYHLIVDKVEFIPIDIQIEKCTKCFEGDICRCGVQSLETKEIVNS 668
Db 630 DQIRLTIEPSFIRQEVYVDRIEFIPV-----PTR-----EAKEDLEAAKAVAS 674
QY 669 LF 670
Db 675 LF 676

RESULT 7

US-09-668-650-10
; Sequence 10, Application US/09668650
; Patent No. 6780408

GENERAL INFORMATION:
APPLICANT: Bosch, Hendrick J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 678040artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/668,650
FILING DATE: 22-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-668-650-10

Query Match 22.5%; Score 801.5; DB 2; Length 1156;
Best Local Similarity 31.2%; Pred. No. 46-67;
Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;

QY 9 NNEYEILDGSPNNTMNS---RYFAPKDPNFPINLDACQRP---WOD-TWESVSDIV 61
DB 2 NQNKGLII-GASNCACADDAVAKYPLANNPYSSALNLSQNSILNWINIIGDAKEAV 60
QY 62 TIGTYLIQFLLEPGIGG-IPVIFSIIINKLI-PSSGQSVAAISICDLVSIIRKEVDESVL 119
DB 61 SIGTTIVSLITAPSLTGLISIVYDLIGVLGGSSGQISDLSICDLLSIIDLRVSQSVLN 120
QY 120 DGVADFEGETAYQDYLYLHLEDWLTDSKNPKLA--DVVKQFQAREEDFTKLL----- 171
DB 121 DGIADFNGLSVLYRN-YLEALDSW---NKNPNASAEELRTFRIDASEFDRITRGSIT 176
QY 172 -AGSLSRQKAEILLPTVYQANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLK 230
DB 177 NGGSLARQNAQILLPLPSASAAFFHLLLRDATRYGTNWG-----LYNATPPIYQSKLV 231
QY 231 AKIKETNYCVGYNKGLDQIRQAGTSAEVSKFNKFRREMTLAVLDIIAIPPTDYFEKY 290
DB 232 ELIELYTDYCVHMYNKGFNELRQGTSAWLEPHRYREMTLWLDIVASFSSLDITNY 291
QY 291 PLATSVELTREIYTPVGY-----SGNYGWERFF---SPNSVEANGTRGPGVLTWQAID 343
DB 292 PIETDFQLSRVIYTDPIGVHRSLSRGESWFSFVRANFSDLE-NAIPNRPSPSWFLNNMI 350
QY 344 IYSHSINLQGLVSG-----WGTREHYEDFTKNGAF--QRMSTTSNNPRNIIFGNTDIF 397
DB 351 ISTGSLTLPVSPSTDRARVWYGSR--DRISPANSOFITELISGQHTATQTILGRN--IF 406

QY 398 KIISLARYAMQPFVGYGYSIPRHLVSRAPFPPTT---LNTFLYE--VNSSGYS-----QTIES 448
DB 407 RVDSOACNLNDTTYG-----VNRVAFYHDASEGSRQSVYGYRTTGTIDNPRVQNIINT 459
QY 449 VLPGLINKDLPPSRNTNYSHRLSNA-----ACVQNETSRVNVFVGWTHTSMKKDNRIYPD 500
DB 460 YLPGENSID-PTPEDYTHILSTINLTGGLRQVANSRSLVMYGWTHKSLARNVTINPD 518
QY 501 KITQIPAVKAFALPAGTGYAGGYVTAGPGYTGDDVVTLPYQASLKLRLTSAPTN--KNYR 558
DB 519 RITQIPLTKVDTRGTGVSYN-----DPGFICALLQRTDHGSLGLVLRVQFPLHLRQQRV 573
QY 559 VRLRYASGPGPFRVERHSPSVSNANFSRPAT-----GGYSSFPYVDVTLVTFNQ 609
DB 574 ITRVYAS-----TTNIRLSVNGSFGTISQNLPSMTLRLGEDLRYGSAIFRENTSIRPTASP 629
QY 610 SGVEIIIO-NLSGYHLVDKVEFIPIDIQIEKCTKQPEGDICRCGVQSLETKEIVNS 668
DB 630 DOIIRTIERSFIRQEVYVDRIEFIPV-----PTR-----BAKEDLEAKKAVAS 674
QY 669 LF 670
DB 675 LF 676

RESULT 8
US-07-876-280-30
Sequence 30, Application US/07876280
Patent No. 5262158
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for
TITLE OF INVENTION: Controlling Acarides
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,280
FILING DATE: 19920430
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C

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; IMMEDIATE SOURCE:
; CLONE: E. coli NM522(pMYC2320) NRRL B-18769
; US-07-876-280-30

Query Match          21.7%; Score 773; DB 1; Length 1157;
Best Local Similarity 30.5%; Pred. No. 2.2e-64;
Matches 224; Conservative 126; Mismatches 265; Indels 120; Gaps 31;

QY 6 SYONTNEYELDGSPNN--TNMSNRYPPAKDPNIPINLDACQRPWQD-----TWESVS 58
Db 2 SPNNQNEYEIIDATPSTSVSSDSNRYPFANEPT-----DALQNMNYKDYLMKSGGENPE 55
QY 59 DIVTIGTYLIQFLLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAAALS 102
Db 56 LFGNPETFISSSTIQTGIGIVGRILGALGVFFASQIASFYFVGLWPKSVVDIWEIM 115
QY 103 CDLVSIIRKEVDSEVSLSDGVADPEGEMTAQDYVYLHYLEDWLTDKSNPKKLADVVKQFOA 162
Db 116 ERVEELVDQKIEKYVKDKALAEKLGKLNAL-DVYQOSLEWLENRDARTSRVSVNQFIA 174
QY 163 REEDFTKLAGSLRSOKAEILLPTVYQAAVHLLLRDAVKYKKEWGLVCPPLPGSGR 222
Db 175 LDINFVSSIP-SPAVSGHEVLLAVYAQAANVHLLLRDASIFGEENGFT-----PGEIS 228
QY 223 TDCNERLKAKIEYTNKCYGVNKGDLQIRQAGTSABVMSKFNKFRREMTLAVLDIAIF 282
Db 229 RFYNRQVQL-TAEYSDYCVKWKYKIGLDKLGK--GTTSKSLNHYHOFREMTLLVLDLVALF 285
QY 283 PTYDFEKYPLATSVELTREIYTPDVG-----SGNYGWERF--FSFNSVEANGTRGPGL 335
Db 286 PNYDTHMYPIETTAQTRDVTDPDIAFNIVTSTGFCNPWSTHSGILFYEVNNVIRPPLH 345
QY 336 VTWLOAIDYSHSINLQ---GYLSGKG--TRHYEDFTKNGAFQRMSTGTTNNPNIIF 391
Db 346 FOILSSVEINTSRGGITLNDAYINYWSGHTLKRYRTADSTVITYTANYGRITSEKNSPAL 405
QY 392 GNTDIFPKIIS----LARYAMQPFGVYSIPR---HLVSRABEFPFTTLNTFLYEVNSS---G 441
Db 406 EDRDIFEINSTANLANYQK---AYGVPGSFWHMVKG---TSSYAYLYSKYTHALQG 459
QY 442 YSQTIIESVLPGINKDLPSPRT-----NYSHRLSNAACVQNETSRVN-----VFGWT 487
Db 460 CTQVYES-----SDEIPLDTPVAESYSHRLSH---ITSHSPSKNGSAVYSGFPFVMT 511
QY 488 HTSMKKDNRIYDKITQIIPAVKAFALPAGTGAGGYVYTAGPGVTGDDV--TLPYQASLK 545
Db 512 HTSADLNNTIYDKITQIIPAVKGMDL-----YLGGSVVQPGPTGGDILKRTNPSILGTF 566
QY 546 IRLTSAPTNNKRVRLRYASGGPGPFPRVERWSPSSVSNANFSRPATGG---YSSFDYVD 601
Db 567 AVTVNGSLSQRVIRIRYAS--TTDPEFTLYLGDITIEKRNFKNTMDNGASLTYYETPKFAS 624
QY 602 TLVLT-TFNGSGVEIITQN---LSGYHLIVKVEFIPIDIQIEKCTKQCEGDCRCGQV 657
Db 625 FITDFQFRTQDKILLSMGDFSGQGVYIDRIEFIPVDETY-----EAEQ 669
QY 658 SLETKKEIVNSLFIN 672
Db 670 DLEAAKAVNALFTN 684

RESULT 9
US-07-812-180A-2
; Sequence 2, Application US/07812180A
; Patent No. 5366892
; GENERAL INFORMATION:
; APPLICANT: Focerrada, Luis R
; APPLICANT: Payne, Jewel M
; APPLICANT: Sick, August J
; TITLE OF INVENTION: No. 5366892el Coleopteran-Active Bacillus
; TITLE OF INVENTION: Thuringiensis Isolate and a No. 5366892el Gene Encoding a
; TITLE OF INVENTION: Coleopteran-Active Toxin
; NUMBER OF SEQUENCES: 2
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Roman Saliwanchik
; STREET: 2421 N.W. 41st Street, Ste A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19920102
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, Roman
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE:
; LIBRARY: Lambdagem (TM) - 11 LIBRARY OF LUIS
; CLONE: 50C
; US-07-812-180A-2

Query Match          21.7%; Score 773; DB 1; Length 1157;
Best Local Similarity 30.5%; Pred. No. 2.2e-64;
Matches 224; Conservative 126; Mismatches 265; Indels 120; Gaps 31;

QY 6 SYONTNEYELDGSPNN--TNMSNRYPPAKDPNIPINLDACQRPWQD-----TWESVS 58
Db 2 SPNNQNEYEIIDATPSTSVSSDSNRYPFANEPT-----DALQNMNYKDYLMKSGGENPE 55
QY 59 DIVTIGTYLIQFLLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAAALS 102
Db 56 LFGNPETFISSSTIQTGIGIVGRILGALGVFFASQIASFYFVGLWPKSVVDIWEIM 115
QY 103 CDLVSIIRKEVDSEVSLSDGVADPEGEMTAQDYVYLHYLEDWLTDKSNPKKLADVVKQFOA 162
Db 116 ERVEELVDQKIEKYVKDKALAEKLGKLNAL-DVYQOSLEWLENRDARTSRVSVNQFIA 174
QY 163 REEDFTKLAGSLRSOKAEILLPTVYQAAVHLLLRDAVKYKKEWGLVCPPLPGSGR 222
Db 175 LDINFVSSIP-SPAVSGHEVLLAVYAQAANVHLLLRDASIFGEENGFT-----PGEIS 228
QY 223 TDCNERLKAKIEYTNKCYGVNKGDLQIRQAGTSABVMSKFNKFRREMTLAVLDIAIF 282
Db 229 RFYNRQVQL-TAEYSDYCVKWKYKIGLDKLGK--GTTSKSLNHYHOFREMTLLVLDLVALF 285
QY 283 PTYDFEKYPLATSVELTREIYTPDVG-----SGNYGWERF--FSFNSVEANGTRGPGL 335
Db 286 PNYDTHMYPIETTAQTRDVTDPDIAFNIVTSTGFCNPWSTHSGILFYEVNNVIRPPLH 345
QY 336 VTWLOAIDYSHSINLQ---GYLSGKG--TRHYEDFTKNGAFQRMSTGTTNNPNIIF 391
Db 346 FOILSSVEINTSRGGITLNDAYINYWSGHTLKRYRTADSTVITYTANYGRITSEKNSPAL 405
QY 392 GNTDIFPKIIS----LARYAMQPFGVYSIPR---HLVSRABEFPFTTLNTFLYEVNSS---G 441
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Db 406 EDRDIFFEINSTVANLANYQK---AYGPGSWFHVKRG---TSSTAYLYSKTHALQG 459
Qy 442 YSQTIESVLPKINGKDLPPSRT-----NYSHRLSNAACVQNETSRVN-----VFGWT 487
Db 460 CTQVYES-----SDEPLDRTVPVAESYSHRLSH---ITSHSFSKNGSAVYGSFPFVMT 511
Qy 488 HTSMKKNRIYDPDKITQIPAVKAFALPAGTGYAGGYVTTAGCYTGGDVV--TLPYQASLK 545
Db 512 HTSADLNNTIYSDKITQIPAVKGDML-----YLGGSVVOGPGFTGGDILKRTNPSILGTF 566
Qy 546 IRLTSAPTNNKYRVLRYASGGPGPRVERWSPSSVSNANFSRATG---YSSFDYVD 601
Db 567 AVTVNGSLSQRYVRIRYAS--TTDFEFTLYLGDTEKRNFKNTMDNGASLTETPKFAS 624
Qy 602 TLVT-TFNQSGVEIION---LSGYHLIVDKVEFIPIDQIEKCTKQCFEGDICRCEGVQ 657
Db 625 FITDFQFRETQDKILLSMGDFSSGQEVYIDRIEFIPVDETY-----EAEQ 669
Qy 658 SLETKKEIVNSLFIN 672
Db 670 DLEAAKAVNALFTN 684

RESULT 10

US-08-315-468-2

; Sequence 2, Application US/08315468

; Patent No. 5554534

; GENERAL INFORMATION:

; APPLICANT: Michaels, Tracy Ellis

; APPLICANT: Foncecra, Luis

; APPLICANT: Narva, Kenneth E.

; TITLE OF INVENTION: Process for Controlling Scarab Pests

; TITLE OF INVENTION: with Bacillus thuringiensis Isolates

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/315,468

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/014,941

; FILING DATE: 01 FEB 1993

; APPLICATION NUMBER: 07/828,430

; FILING DATE: 30-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/808,316

; FILING DATE: 16-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Saliwanchik, David R.

; REGISTRATION NUMBER: 31,794

; REFERENCE/DOCKET NUMBER: MA73.C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 904-375-8100

; TELEFAX: 904-372-5800

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1157 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE:
; LIBRARY: Lambdagem (TM) - 11 LIBRARY OF LUIS FONCERRADA
; CLONE: 50C(a)
; US-08-315-468-2

Query Match 21.7%; Score 773; DB 1; Length 1157;
Best Local Similarity 30.5%; Pred. No. 2.2e-64;
Matches 224; Conservative 126; Mismatches 265; Indels 120; Gaps 31;

Qy 6 SYONTNEYBILDGSPNN--TNMNRYPFAKDNIPFINLDACQRPWQD-----TWESVS 58
Db 2 SPNNQNEYEIIDATPSTSVSDSNRYPFANEPT-----DALQNMVYKDYLMKSGGENPE 55
Qy 59 DIVTIGTYLIQFLLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAAISI 102
Db 56 LFGNPETFISSSTIQTGIGIVGRILGALGVFPASQIASFYSTIVGQLWPSKSYVDIWEIM 115
Qy 103 CDLVSIIRKEVDESVLSDGVADFEGETAYQDYVYHLHLEWLTDKGNPKKLADVWQFOA 162
Db 116 ERVEELVDOKIEKYVDKALAEKGLGNAL-DVYQOSLEDWLENRDARTSRVSVNQFIA 174
Qy 163 REEDFTKLAGSLSRQKAEILLPTVVOAANVHLLLRDAVKYKKGWGLVCPPLYPGSGR 222
Db 175 LDNLNFVSSIP-SFAVSGHEVLLAVYAQAVNLHLLLRDASIFGEWGT-----PGEIS 228
Qy 223 TDCNERLKAKIEYNYCVGWNKGLDQIRQAGTSABVWSKFNKPREMTLAVLDIIAIF 282
Db 229 RPYNRQVQL-TAEYSDYCVKWKIGLDKLG--GTTSKSWLNHYHQFREMTELLVLDLWALF 285
Qy 283 PTYDFEKYPLATSVELTRIETDPVGY-----SGGNYGWERP--PSFNSVEANGTRGPGL 335
Db 286 PNIDTMYPIETTAQUTRDYVTDPIAFNIVTSGFCNPWSTHSGILFYEVENNVIIRPHL 345
Qy 336 VTWLOAIDIYSHSINLQL---GYLSGWWG--TRHYEDFTKNGAFAFORMSGTTSNNPRNIIF 391
Db 346 FDLSSVEINTSRGGITLNDAYINWYSGHTLKYRTADSTVITYTNYGRITSEKNSFAL 405
Qy 392 GNTDIFKIIIS-----LARYAMQPFVGYISIP---HLVSRAEFFPTTNTFLIYEVNSS---G 441
Db 406 EDRDIFEINSTVANLANYQK---AYGPGSWFHVKRG---TSSTAYLYSKTHALQG 459
Qy 442 YSQTIESVLPKINGKDLPPSRT-----NYSHRLSNAACVQNETSRVN-----VFGWT 487
Db 460 CTQVYES-----SDEPLDRTVPVAESYSHRLSH---ITSHSFSKNGSAVYGSFPFVMT 511
Qy 488 HTSMKKNRIYDPDKITQIPAVKAFALPAGTGYAGGYVTTAGCYTGGDVV--TLPYQASLK 545
Db 512 HTSADLNNTIYSDKITQIPAVKGDML-----YLGGSVVOGPGFTGGDILKRTNPSILGTF 566
Qy 546 IRLTSAPTNNKYRVLRYASGGPGPRVERWSPSSVSNANFSRATG---YSSFDYVD 601
Db 567 AVTVNGSLSQRYVRIRYAS--TTDFEFTLYLGDTEKRNFKNTMDNGASLTETPKFAS 624
Qy 602 TLVT-TFNQSGVEIION---LSGYHLIVDKVEFIPIDQIEKCTKQCFEGDICRCEGVQ 657
Db 625 FITDFQFRETQDKILLSMGDFSSGQEVYIDRIEFIPVDETY-----EAEQ 669
Qy 658 SLETKKEIVNSLFIN 672
Db 670 DLEAAKAVNALFTN 684

RESULT 11

US-07-941-650A-2

; Sequence 2, Application US/07941650A

; Patent No. 6294184

; GENERAL INFORMATION:

APPLICANT: Uyeda, Kendrick A.
APPLICANT: Bradisch, Gregory A.
TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,650A
FILING DATE: 19920908

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/758,020
FILING DATE: 12-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,112
FILING DATE: 16-JAN-1991

ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC1638), NRRL B-18751
US-07-941-650A-2

Query Match 21.7%; Score 773; DB 2; Length 1157;
Best Local Similarity 30.5%; Pred. No. 2.2e-64;
Matches 224; Conservative 126; Mismatches 265; Indels 120; Gaps 31;
QY 6 SYQNTNEYILGSPNN--TMSNRYPPAKDNIPIINDACQGRWQD-----TWESVS 58
DB 2 SPNNQNEYIIDAITSVSDSNRPYFANEPT-----DALQNNYKDYLMKSGGENPE 55
QY 59 DIVTIGTYLIQFLLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAAISI 102
DB 56 LFGNETTISSTIQTIGIVGRIIGALGVPPASQIASFYSFIVGLWPSKSVDIWGEIM 115
QY 103 CDLVSIIRKVEDSVLSGVDPEGETAYQDYLYHLEDDWLTDSKNPKKLADVVKQFOA 162
DB 116 ERVEELVDQIKYKDKALAKLGLGNAL-DVYQSLDLEWLENDRATRSVSNQFTA 174
QY 163 REEDTKLAGSLSKQAEILLPTVQANVHLLLRDAVKYKKEWGLVCPPLYPGSGR 222
DB 175 LDNFVSSSTP-SFAVSGHEVLLAVYAQAVNLHLLLRDASIFGEWGT-----PGEIS 228
QY 223 TDCNERLAKIKEYTNYCVGWTNKGDLQIDRQAGTSAEWSKFNKFRRENTLAVLDIIAIF 282

DB 229 RFVNRQVL-TAEYSDYCVKWKYKIGLDK-LK-GTTSKSLNHYHQFRREMTLLVLDLVALF 285
QY 283 PTYDFEKYPLATSVELTREIYTDVGY-----SGNGYWERF--FSFNSVEANGTRGPGL 335
DB 286 PNYDTHMYPIETTAQLTRDVTYDPIAFNIVTSTGFCNFWSTHSGILFYEVENNVRPPHL 345
QY 336 VTMLQAIDYSHSINLQ---GYLSGKG--TRHYEDFTKNGCAFQRMSTGTTNNPRNIIF 391
DB 346 FDLSSVEINTSRGITLNDAYINYSGHTLKVRRTADSTVYTYANTYGRITSEKNSPAL 405
QY 392 GNTDIFKILS---LARYAMQPFVGYISIPR---HLVSRABFFPTTLNTFLYEVNSS---G 441
DB 406 EDRDIFEINSTVANLANYQK---AYGVGSMFWHVKRG---TSSTTAYLYSKHTHTALQG 459
QY 442 YSQTIESVLPKINKDLPPSRT-----NYSHRLSNAACVQNETSRVN-----VFQWT 487
DB 460 CTQVYES-----SDEIFLDRTPVAESYSHRLSH---ITSHSFKNKSGSAYTYGSFPFVMT 511
QY 488 HTSMKKNRIYDPDKITQIPAKAFALPAGTGYAGGYTAGPGYTGDDV---YSSFDVVD 601
DB 512 HTSADLNTIYSDKITQIPAVKGM---YLGGSVVGQGFSGDILKRTNPSILGTF 566
QY 546 IRLTSAPTNNRYRVRLYASGPGPFPRVERWSPSSVSNANFSRDPATGG---YSSFDVVD 601
DB 567 AVTVNGSLSQRYRVRIRYAS--TTDFEFTLYLGTIEKRNKNTMDNGASLTETFKFAS 624
QY 602 TLVT-TFNQSGVEIION---LSGYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCEGVQ 657
DB 625 FITDFQFRETQDKILLSMGDFSSQGEVYIDRIEPIVDETY-----EABQ 669
QY 658 SLETKKEIVNSLFIN 672
DB 670 DLEAAKAVNALEFTN 684

RESULT 12

US-08-100-709-4
Sequence 4, Application US/08100709
Patent No. 5322687

GENERAL INFORMATION:
APPLICANT: Donovan, William P.

APPLICANT: Tan, Yiping

APPLICANT: Jany, Christine S.

APPLICANT: Gonzalez Jr., Jose M.

TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5

TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

ADDRESSEE: Nadel

STREET: 1601 Market Street, 36th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/100,709

FILING DATE: 19930729

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Egoif, Christopher

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205-49

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-757-1590

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 1229 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-100-709-4

Query Match 21.7%; Score 772.5; DB 1; Length 1229;
 Best Local Similarity 32.1%; Pred. No. 2.7e-64;
 Matches 229; Conservative 126; Mismatches 246; Indels 113; Gaps 30;

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QY 11 NEYEILD--GSPNNTNMSNRYPFAKDPNIFPI-----NLDACQGRPWQDTWESVSDIV 61
DB 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCAEVNND-----PFVSA-STVQTGI 60

QY 62 TIGTYLIQFLLEPGIGGIPVIPS-IINKLIPSSGQSVAAALSICDLVSIIRKEYDESVLSD 120
DB 61 NIAGRILGVLPFGAGQLASFYSFLVGELWP-SGRDPWEIFLHVQLIRQOVTENTRNT 119

QY 121 GVADPEGEMTAYQDYLYHLEMDLTKSNPKKLADVVQFQAREEDFTKLLAGSLR-QK 179
DB 120 AIARLEGLGRGVSQ-QALETWLDNRNDARSIIILERYVALELDITTAI--PLFRIN 176

QY 180 AEIILLPTVQANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLKAKIK---EY 236
DB 177 BEVPLLMVYAQAANLHLLLRDASLFGSEWGM-----ASSDVNYQEQIRYTEY 227

QY 237 TNYCVGWNKGLDQIRQAGTSAEVMSKFNKFERMTLAVLDIIAIPPTYDFEYPLATSV 296
DB 228 SNHCQVNTYGLNLR--GTNAESWLRYNQFRDLTLGLVDLVALFPSTYDTRYPINTSA 285

QY 297 ELTREIYDTPVGYSGNYGM--ERFF-----SFNSVEANGTRGPGVLTWLQADIIYSHSI 349
DB 286 QLTREIYDTPIGRTNAPSFGFASTNWNNAFSAIEAIFRPHLLDPPEQLTIYSAS- 344

QY 350 NLQGLVSGWGTTHYEDFTKNGAPORMSGT-----TSNPNRIIFGNITDIFK 398
DB 345 -----SRWSSTQHMNYVWGHRLNFRPIGGTLNTSTQGLTNTNTSINPVTLOFTSRDYR 397

QY 399 IISLARYAMQPFVGYSI PRHLSRAEF-PPTTLNTFLYEVNSSGYSTIESVLPGI--- 453
DB 398 TESNA-----GTNLTFTPVNGVPWFARFNINQON--IYERGATTYQPGV--GLQF 449

QY 454 -NKDLPPSRT-----NYSHRLSNAACVQNETSRVNVFGWHTSMKKNRIYDPKITQIP 506
DB 450 SETELPPETTERPNYESYSHRLSHIGLIIGNTLRAPVYSWTHRSADRTNIGPNRIQIP 509

QY 507 AVKAFALPAGTGYAGGYTAGPGYTGDDVVTLPYQASL-KIRLT-SAPTNKNRVRRLRYA 564
DB 510 LVKALNL-----HSGVTVVGFGFTGGDILRNTGTGTGDIIRLNINVLPSQRYRIRYA 564

QY 565 SGGPGPFRRVWSPSSVSNANFSRPATGG-----YSSFDYVDLTVTFFN---QSGVEIII 616
DB 565 STTDLQF-FTRINGTTVGNFSRTNRGNDLNEYRSFRTAG-PSIPFNFLNAQSTFTLGA 622

QY 617 QNLGSHLVKDFEIPIDIQIEKTKQFEGDICEGQVQSLETKKEIVNSLP 670
DB 623 QSFNSQEVYIDRVFVPAEVT-----EAYDILERAQKAVNALF 661

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RESULT 13

US-08-176-865-4

Sequence 4, Application US/08176865

Patent No. 5616319

GENERAL INFORMATION:

APPLICANT: Donovan, William P.

APPLICANT: Tan, Yiping

APPLICANT: Jany, Christine S.

APPLICANT: Gonzalez Jr., Jose M.

TITLE OF INVENTION: BACILLUS THURINGIENSIS CYTET4 AND CYTETS

TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

ADDRESSEE: Nadel
 STREET: 1601 Market Street, 36th Floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/176,865
 FILING DATE: 30-DEC-1993

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/100,709

FILING DATE: 29-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Egoie, Christopher

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205-49

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-757-1590

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1229 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-176-865-4

Query Match 21.7%; Score 772.5; DB 1; Length 1229;

Best Local Similarity 32.1%; Pred. No. 2.7e-64;

Matches 229; Conservative 126; Mismatches 246; Indels 113; Gaps 30;

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QY 11 NEYEILD--GSPNNTNMSNRYPFAKDPNIFPI-----NLDACQGRPWQDTWESVSDIV 61
DB 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCAEVNND-----PFVSA-STVQTGI 60

QY 62 TIGTYLIQFLLEPGIGGIPVIPS-IINKLIPSSGQSVAAALSICDLVSIIRKEYDESVLSD 120
DB 61 NIAGRILGVLPFGAGQLASFYSFLVGELWP-SGRDPWEIFLHVQLIRQOVTENTRNT 119

QY 121 GVADPEGEMTAYQDYLYHLEMDLTKSNPKKLADVVQFQAREEDFTKLLAGSLR-QK 179
DB 120 AIARLEGLGRGVSQ-QALETWLDNRNDARSIIILERYVALELDITTAI--PLFRIN 176

QY 180 AEIILLPTVQANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLKAKIK---EY 236
DB 177 BEVPLLMVYAQAANLHLLLRDASLFGSEWGM-----ASSDVNYQEQIRYTEY 227

QY 237 TNYCVGWNKGLDQIRQAGTSAEVMSKFNKFERMTLAVLDIIAIPPTYDFEYPLATSV 296
DB 228 SNHCQVNTYGLNLR--GTNAESWLRYNQFRDLTLGLVDLVALFPSTYDTRYPINTSA 285

QY 297 ELTREIYDTPVGYSGNYGM--ERFF-----SFNSVEANGTRGPGVLTWLQADIIYSHSI 349
DB 286 QLTREIYDTPIGRTNAPSFGFASTNWNNAFSAIEAIFRPHLLDPPEQLTIYSAS- 344

QY 350 NLQGLVSGWGTTHYEDFTKNGAPORMSGT-----TSNPNRIIFGNITDIFK 398
DB 345 -----SRWSSTQHMNYVWGHRLNFRPIGGTLNTSTQGLTNTNTSINPVTLOFTSRDYR 397

QY 399 IISLARYAMQPFVGYSI PRHLSRAEF-PPTTLNTFLYEVNSSGYSTIESVLPGI--- 453
DB 398 TESNA-----GTNLTFTPVNGVPWFARFNINQON--IYERGATTYQPGV--GLQF 449

QY 454 -NKDLPPSRT-----NYSHRLSNAACVQNETSRVNVFGWHTSMKKNRIYDPKITQIP 506
DB 450 SETELPPETTERPNYESYSHRLSHIGLIIGNTLRAPVYSWTHRSADRTNIGPNRIQIP 509

QY 507 AVKAFALPAGTGYAGGYTAGPGYTGDDVVTLPYQASL-KIRLT-SAPTNKNRVRRLRYA 564

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Db 510 LKALML-----HSGVTGPGFTGCDILRRNTTGTGDIRLNINVLPSQRVRIRYA 564
Qy 565 SGGPGFRVERMSPSSVSNANFRPATGG-----YSSFDYVDTLVTFN-----OSGVEIII 616
Db 565 STTDLOF-FTRINGTIVNIGNSRTNRGDNLEYSFRTAG-FSTPFNLAQSTTLGA 622
Qy 617 QNLGSHLIVDKVEFIPIDIQIEKTKCQPEGDCRCEGVQSLETKKEIVNSLF 670
Db 623 QSPSNOEVYIDRVFVPAEVT-----EAYDLERAKAVNALF 661

RESULT 14
US-08-474-038-4
; Sequence 4, Application US/08474038
; Patent No. 5679343
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYETS
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,038
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,865
; FILING DATE: 30-DEC-1993
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match 21.7%; Score 772.5; DB 1; Length 1229;
Best Local Similarity 32.1%; Pred. No. 2.7e-64;
Matches 229; Conservative 126; Mismatches 246; Indels 113; Gaps 30;

Qy 11 NEVEILD--GSPNNTNMSNRYPPAKDPNIFPI-----NLDAQCRPMDTWESVSDIV 61
Db 7 NENEIINALSITVSNPSTQMLSPDARIEDSLCVAEVNID-----PFVSA-STVTGI 60
Qy 62 TIGTYLIQFLBPGIGGIVPFS-IINKLIPSGQSAALSICDLVSIIRKXEVDSVLSD 120
Db 61 NIAGRILGLVGPFAQLASFSYFLVGLWP-SGRDPWEIFLHVQLIRQQVTENTRT 119
Qy 121 GVADFEGETATQDYLYLHYLEDWLTDSNPKKLADVVVKQFOAREEDFTKLAGSLR-QK 179
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Db 120 AIALREGLGRGYSYQ-QALETWLDNRDARSRSIILERYVALELDITTAI--PLFIRRN 176
Qy 180 AEIILLPTVYQAAANVHLLLRDAVKYKKEGLVCPPLYPGSGRTDCNERLKAKIK---EY 236
Db 177 EEPVLLMVYQAAANVHLLLRDASLFGSEWGM-----ASSDVNQYQEIRYTRYEY 227
Qy 237 TNYCVGMYNKLQDIOIRQAGTSAEYVMSKFNPRREMTLAVLDIIAIFPTYPDEKYPATSV 296
Db 228 SNHCVQWYNTGLNNLR--GTNAESWLRYNQFRDLTLGLVDLVALFPSYDTRTYPINTSA 285
Qy 297 ELTREIYTDVPYSGGNYGM--ERFF-----SPNSVEANGTRGCLVTLWQAIDYISHSI 349
Db 286 QLTREIYTDPIGRTNAPSGFASTNMFNNAPSPAIEAAIFRPHLLDFPEQLTIYSAS- 344
Qy 350 NLQGLYLSGWSGGRHYEDFTKGCAFORMSGT-----TSNNPRNIIFGWTDIFK 398
Db 345 -----SRWSTQHMYVWGHRLNFRPIGGTLNTSTOGLTNTSINPVTIQTSDRDVTR 397
Qy 399 IISLARYAMQPFVGYISIPRHLVSRAEF-FPTTLNTFLYEVNASSGYSTIESVLPGI---- 453
Db 398 TESNA-----GTNIIFTTPVNGVPWARFNPNQ--IYERGATTVSQPVQGV--GLQLPD 449
Qy 454 -NKDLPPSRT-----NYSHRLSNAACVQNETSRVNVFGWTHSTMKDNRIYDPKITQIP 506
Db 450 SETELPPETTERPNYESYSHRLSHIGLIIGNTLRAPVYSWTHRSADRTNTICPNRITQIP 509
Qy 507 AVKAFALPACTGYAGGVYTAGRGYTGDDVTLPYQASL-KIRLT-SAPTNNKRYRVLRYA 564
Db 510 LVRALNL-----HSGVTGPGFTGCDILRRNTTGTGDIRLNINVLPSQRVRIRYA 564
Qy 565 SGGPGFRVERMSPSSVSNANFRPATGG-----YSSFDYVDTLVTFN-----OSGVEIII 616
Db 565 STTDLOF-FTRINGTIVNIGNSRTNRGDNLEYSFRTAG-FSTPFNLAQSTTLGA 622
Qy 617 QNLGSHLIVDKVEFIPIDIQIEKTKCQPEGDCRCEGVQSLETKKEIVNSLF 670
Db 623 QSPSNOEVYIDRVFVPAEVT-----EAYDLERAKAVNALF 661

RESULT 15
US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYETS
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-046-4

Query Match      21.7%; Score 772.5; DB 1; Length 1229;
Best Local Similarity 32.1%; Pred. No. 2.7e-64;
Matches 229; Conservative 126; Mismatches 246; Indels 113; Gaps 30;

QY      11 NEYEILD--GSPNNTNMSNRYPPFAKDPNIFPI-----NLDACQGRPWQDTWESVSDIV 61
DB      7 NENEIINALSIPTVSNPTQNMLSDPARIEDSLCVAENVNID-----PFVSA-STVQTGI 60

QY      62 TIGTYLQFLLEPGIGGIPVIFS-IINKLIPSSGOSVAALSICDLVSIIRKEVDESVLSD 120
DB      61 NIAGRILGVLPVPPAGQLASFYSFLVGLWLP-SGRDPWEIFLHVQLIRQQVTENTNT 119

QY      121 GVADPEGEMTAYQDYLYLHLEDWLTDKSNPKKLADVVKQFOAREDEFTKLAGLSLR-QK 179
DB      120 AIALLEGILGRGYSYQ-QALETWLDNRDARSIIILERYVALELDITTAI--PLFRIRN 176

QY      180 AEILLPTVQAANVHLLLDRAVKYKKEWGLVCPPLYPGSGRTDCNERLKAQK---EY 236
DB      177 EEVLLMVAQAANLHLLLRDASLFGSEWGN-----ASSDVNQYQEQIRYTEEY 227

QY      237 TNYCVGYNKGLDQIROAGTSAEVMSKFNKFEREMTLAVLDIIAIFPTVDPEKYPLATSV 296
DB      228 SNHCQWNTGNLNR--GTNAESWLRYNQFARDLTGLVLDLVALFPSTYDTFTYINTSA 285

QY      297 ELTREIYTDVPVYSGGNYGW--ERFF-----SFNSVEANGTRGPGLVTLWLQALDIYSHSI 349
DB      286 QLTREIYTDPIGRTNAPSGFASTNWFNNAPSAIEAAI FRPHLLDPPEQLTIYSAS- 344

QY      350 NLQGLYSCWGGTRHYEDFTKNGAFQMSGT-----TSNNPRNIIFGNTDIFK 398
DB      345 -----SRWSSTQHMNTVWGHRLNFRPIGGTLNTSTQGLTNNTSINPVTLOFTSRDVYR 397

QY      399 IISLARYAMQPFVGYSI PRHLVRAEF-FPTLTNTFLYVNSSGYSQTESVLPGI---- 453
DB      398 TESNA-----GTNILETTPVNGVPWAFNFINPON--IYERGATTYSQPYQGV--GIQLFD 449

QY      454 -NKDLPPSRT-----NYSRLSNAACVQNETSRVNVFGWTHSTMKKNRIYPDKITQIP 506
DB      450 SETELPPETTERPNYESYSHRLSHIGLIIGNTLRAPVYSWTHRSADRTNTIGPNRITQIP 509

QY      507 AVKAFALPAGTGYAGGYTAGCYTGGDVVTLPYQASL-KIRLT-SAPTNKRYRVLRYA 564
DB      510 LVKALNL-----HSGVTYVGGFGTGGDILRNTGTGDIRLININPLSORVRYRYA 564

QY      565 SGCGPFRFRWSPSSVANFSRATGG---YSSFDYVDVLTFTEN---QSGVEIII 616
DB      565 STTDLPQ-FTRINGTIVNIGFSRTRWNGDNLEYSFRTAG-FSTFFFLNAQSTFTIGA 622

QY      617 QNLGGYHLIVDKVEFIPIDIQIEKTKQCFEGDICRCBGVQSLETKKEIVNSLF 670
DB      623 QSFNQEVVIDRVEFVPAEVT-----EAEYDLERAQKAVNALF 661
```

Search completed: December 15, 2005, 10:20:21
Job time : 51 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2005, 10:11:18 ; Search time 78 Seconds
(without alignments)

3599.760 Million cell updates/sec

Title: US-10-782-141-3

Perfect score: 3556

Sequence: 1 MKNMNSYQNTNEYILDGSP.....CEGVQSLETKKEIVNSLFIN 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3556	100.0	672	4	US-10-782-141-3
2	3540	99.6	669	4	US-10-782-141-5
3	1872	52.6	666	4	US-10-782-141-23
4	1872	52.6	666	4	US-10-782-096-23
5	1872	52.6	666	5	US-10-781-979-25
6	1571.5	44.2	693	5	US-10-781-979-3
7	1561.5	43.9	690	5	US-10-781-979-5
8	918.5	25.8	674	4	US-10-782-141-20
9	918.5	25.8	674	4	US-10-782-096-21
10	918.5	25.8	674	4	US-10-782-570-17
11	918.5	25.8	674	5	US-10-783-417-15
12	918.5	25.8	674	5	US-10-781-979-22
13	833.5	23.4	682	4	US-10-782-096-2
14	801.5	22.5	1151	6	US-11-018-615-13
15	801.5	22.5	1156	4	US-10-099-285-70
16	801.5	22.5	1156	6	US-11-018-615-12
17	782.5	22.0	671	4	US-10-782-096-4
18	776.5	21.8	1210	4	US-10-032-717-4
19	776.5	21.8	1210	4	US-10-414-637-4
20	776.5	21.8	1210	4	US-10-606-320-4
21	776.5	21.8	1210	4	US-10-746-914-4
22	773	21.7	1157	4	US-10-782-141-16
23	773	21.7	1157	4	US-10-782-096-17
24	773	21.7	1157	4	US-10-782-570-13
25	773	21.7	1157	5	US-10-783-417-11
26	773	21.7	1157	5	US-10-781-979-18
27	773	21.7	1157	5	US-10-926-819-15

28	770.5	21.7	802	4	US-10-428-961-30	Sequence 30, Appl
29	765.5	21.5	661	4	US-10-782-096-6	Sequence 6, Appl
30	765	21.5	1167	4	US-10-089-678-1	Sequence 1, Appl
31	756.5	21.3	719	5	US-10-926-819-30	Sequence 30, Appl
32	756.5	21.3	719	5	US-10-926-819-31	Sequence 31, Appl
33	756	21.3	1228	5	US-10-926-819-8	Sequence 8, Appl
34	754.5	21.2	1206	4	US-10-032-717-2	Sequence 2, Appl
35	754.5	21.2	1206	4	US-10-414-637-2	Sequence 2, Appl
36	754.5	21.2	1206	4	US-10-606-320-2	Sequence 2, Appl
37	754.5	21.2	1206	4	US-10-746-914-2	Sequence 2, Appl
38	754	21.2	1228	4	US-10-809-953-10	Sequence 10, Appl
39	752	21.1	667	4	US-10-032-717-8	Sequence 8, Appl
40	752	21.1	667	4	US-10-414-637-8	Sequence 8, Appl
41	752	21.1	673	4	US-10-032-717-18	Sequence 18, Appl
42	752	21.1	673	4	US-10-414-637-18	Sequence 18, Appl
43	752	21.1	673	4	US-10-606-320-14	Sequence 14, Appl
44	752	21.1	673	4	US-10-746-914-14	Sequence 14, Appl
45	746.5	21.0	1207	3	US-09-988-462-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-10-782-141-3

; Sequence 3, Application US/10782141

; Publication No: US20040197917A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Koziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and

; FILE OF INVENTION: Methods for Its Use

; FILE REFERENCE: 045600/274143

; CURRENT APPLICATION NUMBER: US/10/782,141

; CURRENT FILING DATE: 2004-02-20

; PRIOR APPLICATION NUMBER: 60/448,632

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 672

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

; US-10-782-141-3

Query Match 100.0%; Score 3556; DB 4; Length 672;
Best Local Similarity 100.0%; Pred. No. 5.2e-304; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKNMNSYQNTNEYILDGSPNTNMNSRYPFAKDPNIPFNLDACQGRPWQDTWESVSDI	60
DB	1	MKNMNSYQNTNEYILDGSPNTNMNSRYPFAKDPNIPFNLDACQGRPWQDTWESVSDI	60
QY	61	VTIGTYLIQFLLEPGGIGGIPVPSIINKLIPSSGQSVAAALSICDLVSIIRKEVDESVLSD	120
DB	61	VTIGTYLIQFLLEPGGIGGIPVPSIINKLIPSSGQSVAAALSICDLVSIIRKEVDESVLSD	120
QY	121	GVADPEGEANTQDYLYLHYLEDWLTOKSNPKLADVVKQFQAREEDFTKLLAGLSRQKA	180
DB	121	GVADPEGEANTQDYLYLHYLEDWLTOKSNPKLADVVKQFQAREEDFTKLLAGLSRQKA	180
QY	181	EILLPTTYQAAVNHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNRLKAKIKEYTNYC	240
DB	181	EILLPTTYQAAVNHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNRLKAKIKEYTNYC	240
QY	241	VGWYKGLDQIRQAGTSAEVWSKFNKFRREMTLAVLDIIAIFPTYDFEKPPLATSVELTR	300
DB	241	VGWYKGLDQIRQAGTSAEVWSKFNKFRREMTLAVLDIIAIFPTYDFEKPPLATSVELTR	300
QY	301	EIYTPDVGSGGNYGWERFFSFNSVEANGTRGPGVTLWLOAIDIYSHSINLQLGYSWG	360

```
Db 301 ELYTDPVSGNYGWERFFSFNSVEANGTRGPGVLTWLAQADIIYSHSINLQGLYLSGWG 360
Qy 361 GTRHYEDFTKNGAFQRMSSGTTNNPRNII FGNITDIFKIIISLARVAMQPFVGYSPRHLY 420
Db 361 GTRHYEDFTKNGAFQRMSSGTTNNPRNII FGNITDIFKIIISLARVAMQPFVGYSPRHLY 420
Qy 421 SPAEFPPTLTANTFLYEVNSSGYSOTIESVLPKINLDPSPRTNYSHRLSNAACVQNETSR 480
Db 421 SPAEFPPTLTANTFLYEVNSSGYSOTIESVLPKINLDPSPRTNYSHRLSNAACVQNETSR 480
Qy 481 VNVFGWHTSMKKDNRIYDPDKITQIPAVKAFALPAGTGYAGGVYTAGPGYTGDDVVTLPY 540
Db 481 VNVFGWHTSMKKDNRIYDPDKITQIPAVKAFALPAGTGYAGGVYTAGPGYTGDDVVTLPY 540
Qy 541 QASLKIRLTSAPTNNKYRVRLEYASGGPGPFPRVERWSPSSVSNANFSRPAATGGYSSFDYV 600
Db 541 QASLKIRLTSAPTNNKYRVRLEYASGGPGPFPRVERWSPSSVSNANFSRPAATGGYSSFDYV 600
Qy 601 DTLVTFNQSGVEIIIONLSGYHLIVDKVEFIPIDIIQIEKCTKCOPEGDPCRCEGVQSL 660
Db 601 DTLVTFNQSGVEIIIONLSGYHLIVDKVEFIPIDIIQIEKCTKCOPEGDPCRCEGVQSL 660
Qy 661 TKKEIVNSLFIN 672
Db 661 TKKEIVNSLFIN 672
```

RESULT 2

```
US-10-782-141-5
; Sequence 5, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; CURRENT APPLICATION NUMBER: US/10782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-5
```

```
Query Match 99.6%; Score 3540; DB 4; Length 669;
Best Local Similarity 100.0%; Pred. No. 1.3e-302;
Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 MNSYQNTNEYIILDGSPNNTNMSNRYPPAKDPNIPINLDACQGRPQDWTWESVDIVTI 63
Db 1 MNSYQNTNEYIILDGSPNNTNMSNRYPPAKDPNIPINLDACQGRPQDWTWESVDIVTI 60
Qy 64 GTYLQFLLEPGIGGIPVIFSIIKLIIPSSGQSVAAALSICDLVSIIRKEVDESVLSDGVA 123
Db 61 GTYLQFLLEPGIGGIPVIFSIIKLIIPSSGQSVAAALSICDLVSIIRKEVDESVLSDGVA 120
Qy 124 DFEGETAYQDYLYLHYLEDWLTDKSNPKKLADVVKQFOAREDDFTKLLAGSLSRQAEIL 183
Db 121 DFEGETAYQDYLYLHYLEDWLTDKSNPKKLADVVKQFOAREDDFTKLLAGSLSRQAEIL 180
Qy 184 LLPTVQQAANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNRLKAKIKETNYVCWG 243
Db 181 LLPTVQQAANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNRLKAKIKETNYVCWG 240
```

```
Qy 244 YNKGLDQIRQACTSAEVMKSNKFRREMTLAVLDIIAIFPTDYDFEKYPLATSVELTREIY 303
Db 241 YNKGLDQIRQACTSAEVMKSNKFRREMTLAVLDIIAIFPTDYDFEKYPLATSVELTREIY 300
Qy 304 TDPVGYSGNYGWERFFSFNSVEANGTRGPGVLTWLAQADIIYSHSINLQGLYLSGWGTR 363
Db 301 TDPVGYSGNYGWERFFSFNSVEANGTRGPGVLTWLAQADIIYSHSINLQGLYLSGWGTR 360
Qy 364 HYEDFTKNGAFQRMSSGTTNNPRNII FGNITDIFKIIISLARVAMQPFVGYSPRHLYSRA 423
Db 361 HYEDFTKNGAFQRMSSGTTNNPRNII FGNITDIFKIIISLARVAMQPFVGYSPRHLYSRA 420
Qy 424 EFPPTLTANTFLYEVNSSGYSOTIESVLPKINLDPSPRTNYSHRLSNAACVQNETSRVNV 483
Db 421 EFPPTLTANTFLYEVNSSGYSOTIESVLPKINLDPSPRTNYSHRLSNAACVQNETSRVNV 480
Qy 484 FGWHTSMKKDNRIYDPDKITQIPAVKAFALPAGTGYAGGVYTAGPGYTGDDVVTLPYOAS 543
Db 481 FGWHTSMKKDNRIYDPDKITQIPAVKAFALPAGTGYAGGVYTAGPGYTGDDVVTLPYOAS 540
Qy 544 LKIRLTSAPTNNKYRVRLEYASGGPGPFPRVERWSPSSVSNANFSRPAATGGYSSFDYVDTL 603
Db 541 LKIRLTSAPTNNKYRVRLEYASGGPGPFPRVERWSPSSVSNANFSRPAATGGYSSFDYVDTL 600
Qy 604 VTFNQSGVEIIIONLSGYHLIVDKVEFIPIDIIQIEKCTKCOPEGDPCRCEGVQSL 663
Db 601 VTFNQSGVEIIIONLSGYHLIVDKVEFIPIDIIQIEKCTKCOPEGDPCRCEGVQSL 660
Qy 664 EIVNSLFIN 672
Db 661 EIVNSLFIN 669
```

RESULT 3

```
US-10-782-141-23
; Sequence 23, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; CURRENT APPLICATION NUMBER: US/10782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-23
```

```
Query Match 52.6%; Score 1872; DB 4; Length 666;
Best Local Similarity 57.0%; Pred. No. 1.5e-155;
Matches 392; Conservative 91; Mismatches 161; Indels 44; Gaps 15;
Qy 5 NSYQNTNEYIILDGSPNNTNMSNRYPPAKDPNIPINLDACQGRPQDWTWESVDIVTI 64
Db 1 NSYQNTNEYIILDGSPNNTNMSNRYPPAKDPNIPINLDACQGRPQDWTWESVDIVTI 60
Qy 65 TYILOFLLEPGIGGIPVIFSIIKLIIPSSGQSVAAALSICDLVSIIRKEVDESVLSDGVA 124
Db 61 IDLIEFLMEPLSGGINTLFSIIKLIIPTHQSVSALSICDLVSIIRKEVADSVLSDAICR 120
Qy 125 F-EGEMTAYQDYLYLHYLEDWLT-----XSNPKKLADVVKQFOAREDDFTKLLAGSLSRQ 178
Db 121 FLDGKLKNRYEYLPLEAWLKDGPLOKNTNNSDGLQVVKYFELSRDFNEILGSLARN 180
```



```

Db 1 NSYENKNEYEILESSNNNTNPNRYPFANDRDMSTMFSNDGQISWDEIWESAFTISG 60
Qy 65 TYLQFLLEPGIGIPVIFSIINKLIPSSGQVAALSICDLVSIIRKEVDESVLSDG 124
Db 61 IDLIEFLMEPLSGINTLFSIGKLIPTNHOSVSALSICDLVSIIRKEVADSVLSDA 120
Qy 125 F-EGEMTAYQDYVLYHLEWDLTD-----KSNPKKLADVVVKQFOAREEDFTKL 178
Db 121 FLDGKLNREYLYLLEAWLKDGPLOKTNNSDIGQLVYKIFELSERDFNEILGSL 180
Qy 179 KAEILLLPTVYQAANVHLLLRDAVYKKEW-----GLVCPPLPGSG---RTDC 228
Db 181 NAQILLLPYFCASCQKQLLLLRDAVYEQWPFPLSAENVRSLSNPGCDFTGDYER 240
Qy 229 LKAKIKEYTNYCVGYNKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIFTY 288
Db 241 LKCKIAEYTDYCEWYQAGLNQIKQAGTGADTWAKFNKFRREMTLAVLDIIAIF 300
Qy 289 KYPLATSVELTREIYTDVPGYSGGNYGWERFF--SPNSVEANGTRGPGGLVTWL 346
Db 301 KYPLPHTVELTREIYTDVPGYSSGYTSMWKYWTGAFNTLEANGTRGPGGLVTW 360
Qy 347 HSINLQGLGCGWGTTRHYEDFTKNGAFORMSGTTSNNPRNIIFGNTDIFKII 406
Db 361 EYVS---RYFGWGTTRHYEDFTKNGAFORMSGTTSNNPRNIIFGNTDIFKII 414
Qy 407 MOPFVG--YSTPRHVSRAEPFTTLTFLYEVNSGY--SOTIESVLPKINKDLP 463
Db 415 IMNLVGEINARPEYVSRAEFSESTAFIYLYDAGNSGLSMTTISKLPGI-KNPE 473
Qy 464 YSHRLSNAACVQNETSRVNVFGWTHTSKMDKNRIYDPDKITQIPAKFALPAGT 523
Db 474 YSHRLSNAACVAGNSRNVGVWTHTSKMYNLIYDPDKITQIPAKFALPAGT 530
Qy 524 VTAGPGYTGVDVTLPYQASLKIRLTSAPTNNKYNVRLRYAGGPGPFVERWSP 583
Db 531 VIAGPGHTGNNVSLPYVSRKIRLIPASTNNKYNVRLRYAGGPGPFVERWSP 590
Qy 584 ANFSRPAATGYSFDPVTLTFTNQSGVEIIQNLGSHLIVDKVEFIPIDIEKCT 643
Db 591 SYFFLPSTPGDSFGVDVTLTFTNQSGVEIIQNLGSHLIVDKVEFIPVNV 644
Qy 644 QFEGDICRCEGVQSLTKKEIVNSLFI 671
Db 645 LEYEGK-----QSLKQAQDVVNDLFV 665

```

RESULT 6

US-10-781-979-3

; Sequence 3, Application US/10781979

; Publication No. US20040250311A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Koziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and

; FILE REFERENCE: 045600/274147

; CURRENT APPLICATION NUMBER: US/10/781,979

; PRIOR FILING DATE: 2004-02-20

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 693

; TYPE: PR1

; ORGANISM: Bacillus thuringiensis

US-10-781-979-3

```

Query Match 44.2%; Score 1571.5; DB 5; Length 693;
Best Local Similarity 47.2%; Pred No. 5.1e-129;
Matches 340; Conservative 107; Mismatches 198; Indels 75; Gaps 18;

Qy 1 MKNMNSYQNTWEYELDGSPPNNTNPNRYPFANDRDMSTMFSNDGQISWDEIWESA 60
Db 1 MKNMNSYQNTWEYELDGSPPNNTNPNRYPFANDRDMSTMFSNDGQISWDEIWESA 60
Qy 61 VTIGTYLQFLLEPGIGIPVIFSIINKLIPSSGQVAALSICDLVSIIRKEVDESVL 120
Db 61 TSIGNLNLEFVPELSPGINTLFSIGKLIPTNHOSVSALSICDLVSIIRKEVADS 120
Qy 121 GVADPEGETAYQDYVLYHLEWDLTD-----KSNPKKLADVVVKQFOAREEDFT 175
Db 121 ATADFDGKLNREYLYLLEAWLKDGPLOKTNNSDIGQLVYKIFELSERDFNEIL 180
Qy 176 SRQKAEIILLPTVYQAANVHLLLRDAVYKKEW-----GLVCPPLPGSG--- 225
Db 181 SRNNAQVLLPTFAQAANVQVLLLRDAVYKQWPPFLSAENVRSLSNPGCDFTGDY 240
Qy 226 NERLKAKIKEYTNYCVGYNKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIF 285
Db 241 YERLCKTAETNYCLYWTYQVGLNQIKQAGTGADTWAKFNKFRREMTLAVLDIIA 300
Qy 286 DPEKPLATSVELTREIYTDVPGYSGGNYGWERFF--SPNSVEANGTRGPGGLVT 343
Db 301 DPEKPLPHTVELTREIYTDVPGYSSGYTSMWKYWTGAFNTLEANGTRGPGGLVT 360
Qy 344 IYSHSINLQGLGCGWGTTRHYEDFTKNGAFORMSGTTSNNPRNIIFGNTDIFKII 403
Db 361 IYNEVVS---RYFAGWGTTRHYEDFTKNGAFORMSGTTSNNPRNIIFGNTDIFK 416
Qy 404 RYAMPQFVGYSI--PRHLVSRABEPFTTLTFLYEVNSGY--TIESVLP----- 454
Db 417 --AIMNLVGEINARPEYVSRAEFSESTAFIYLYDAGNSGLSMTTISKLPGI 474
Qy 455 KDLPSRTNYSRLSNAACVQNETSRVNVFGWTHTSKMDKNRIYDPDKITQIPAKF 514
Db 475 -----GPSHRLSNAACVGVNSRVNVGVWTHTSKMDKNRIYDPDKITQIPAK 526
Qy 515 AGTYAGGVTAGPGYTGVDVTLTFTNQSGVEIIQNLGSHLIVDKVEFIPIDIE 564
Db 527 NYLANAYTVVIKGT-HTGDLIRFLRTKSEYNNAVYAGGGLIRLNNKTAQSYRI 585
Qy 565 SGGPGPFVERWSPSSVSN--ANFSRPAATGYSFDPVTLTFTNQSGVEIIQ 617
Db 586 ADKAAFFSYLYPGGWSNRFSVLSKSYSGNYDLDKYSDFKFAEIIITPPLPSSN 645
Qy 618 N-----LSGYHLIVDKVEFIPIDIEKCTKQFEGDICRCEGVQSLTKKEIV 672
Db 646 MQANSFQSDVNVVLDKIEFLP-----SNTTLEYEGE-----RDLEKTKNA 693

```

RESULT 7

US-10-781-979-5

; Sequence 5, Application US/10781979

; Publication No. US20040250311A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Koziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and

; FILE REFERENCE: 045600/274147

; CURRENT APPLICATION NUMBER: US/10/781,979

; PRIOR FILING DATE: 2004-02-20

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

```
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-781-979-5

Query Match      43.9%; Score 1561.5; DB 5; Length 690;
Best Local Similarity 47.1%; Pred. No. 3.8e-128;
Matches 338; Conservative 107; Mismatches 197; Indels 75; Gaps 18;

QY 4 MNSYQNTNEVEILLDGSNNNTMSNRYPPFAKDPNIPFINDACQGRPWQDTWESVDTVTI 63
Db 1 MSYQNKNEYEILLESSNNNTNTPFPANRDMSTMSMNDCCGIDWEIWEVETITSI 60

QY 64 GYLIQFLLEPGIGGIPFISIIINKLIPSGQVAALSIDLVLSIIRKEVDESVLSDGVA 123
Db 61 GINLIEFVIEPSLGGINTLLSIIGKLPTRQTVSALSICDLSIIRKEVADSVLSDAIA 120

QY 124 DFEGETAYQDYLYLHYLEDWLT-----XSNPKKLADVVKVQFQARBEDFTKLALAGSLRQ 178
Db 121 DFDGKLKNRYEYLYSLGAWLKDGKPLQKTNNSDIGOLVYVFKLSERDFNEILGGSLRN 180

QY 179 KAEIILLPTVQAAVHLLLRDAVKYKKEW-----GLVCPPLYPGSG---RTDCNR 228
Db 181 NAQVLLPTFAQAAVQVLLLRDAVQYKQWPFPLSAENVRSLSIPNSGCCDFTGDYER 240

QY 229 LKAKIKEYTNYCVGWYKGLDQIROAGTSAEVMKSKENKFRREMTLAVLDIIAIFPTVDPE 288
Db 241 LACKTAETNYCLYTVQVGLNQIKQGTGADTWSKKNKFRREMTLAVLDIIAIFPTVDPE 300

QY 289 KYPLATSVELTREIYTPDVGYSNGYGFPPF---SFNSVEANGTRGPGVLTWLQADIDYS 346
Db 301 KYPLPHTHVELTREIYTDVAGYSSGYSLWRNPMTENGLEANGTRGPGVLTWLSKIGYN 360

QY 347 HSINLQGLSWGGRHVEDFTKNGAFQRMSTGTSNNPRNIIFGNITDIFKILSARVA 406
Db 361 EYVS---RYFAGVWGTRHVEDYTKNGIFQRMSTGTSNDRNIDFQADVYKITSL---A 414

QY 407 MQPFVGYSI---PRHLVSRAREFPFTTLTFLYEVNSSGYSQ-TIESVLP-----GINKOL 457
Db 415 INMLVGETTARPEYRVSADFRVGGPDNLNVDAGNGLSRMTIESTFFVLVHNSGVR--- 471

QY 458 PPSRTNYSHRLSNAACVQNETSRVNVFGWTHTSMKKDNRIYDPKIQIPAVKAFALPAGT 517
Db 472 -----GPHRLSNAACVYGNRVNYGTHTSLKRENIIEANQIQIPAVKSYLYQNYL 526

QY 518 GVAGGYVTAGYTGDDVVTL-----PYQA-----SLKIRLTSAPTNNKRYVRLRYASGG 567
Db 527 ANAYTVVIKGT-HTGDLIRFLTRKSEYNNAVYAGGIGIRLIINNKTAGQSYRIRFRYAADK 585

QY 568 PGPFVRVERWSPSSVN---ANFSRPATGG-----YSSFDYVDTLVTFNOSGVEIILION-- 618
Db 586 AAFPSVLYPGWGNRFRVLSKSYSGNVDLYKISDFKFAEITTPPLPSNSNIQMDVEMQA 645

QY 619 ---LSGYHLIVDKVEFIPIDIQIEKCTKCFEGDICRCGVSQSLTKKEIVNSLFIN 672
Db 646 NSFQDQVNVLDKIEFLP-----SNTTLEYEGE-----RDLETKNAVNDLFTN 690

RESULT 8
US-10-782-141-20
; Sequence 20, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782,141
; CURRENT FILING DATE: 2004-02-20

; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-20

Query Match      25.8%; Score 918.5; DB 4; Length 674;
Best Local Similarity 33.2%; Pred. No. 1.8e-71;
Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;

QY 4 MNSYQNTNEVEILLDGSNNNTMSNRYPPFAKDPNIPFINDACQGRPWQDTWESV 57
Db 1 MNQYQNKNEYEILLESSQNNMNPYFPADPNAMKNGNYKDWNECEG-----SNISP 55

QY 58 SDIVTIGTYLIQFLLEPGIGGIPFISIIINKLIPSG-----QSVAAALSICDLVSIIR 110
Db 56 SPAAATSKIVSIVLTKLAKA--VASSLADSIKSSLSIGISKITITENNVSQVSMVQVHIIIN 113

QY 111 KEYDESVLSDGVADFEGETAYQDYLYLHYLEDWLTDKSNPKKLADVVKVQFQARBEDFTKL 170
Db 114 RRIQETILDGESSLGLVAIYNRDYLGALEAMNNKSNINYQTNVAEAFKTVREFFTK 173

QY 171 LAGSLSRQAEIILLPTVQAAVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLK 230
Db 174 LKGIYRTSSQITLLPTFTQAAHLHLSMLRDAVMYQEGWNL-----QSHINYSKELD 225

QY 231 AKIKEYTNYCVGWYKGLDQIROAGTSAEVMKSKENKFRREMTLAVLDIIAIFPTVDPEKY 290
Db 226 DALEDVTNYCEVYTTKGLNALR--GSTAIDWLEFNSFRDMTLMVLVDLVAIFPNYPVRY 283

QY 291 PLATSVELTREIYTPDVGYSNGG-NYG-W-----ERFFSFNSVEANGTRGPGVLTWLQADID 344
Db 284 PLSTKISLSRKIYTPDVGRTDPSFGDWTNTGRTLANFNDLEREVTDSPSLVKWLGDMTI 343

QY 345 YHSINLQGLYLSG-----WGTRHVEDFTKNGAFQRMSTGTSNNPRNIIFGN---TD 395
Db 344 YTGAIIDSYRPTSPGDRIGVWYGNINAFYHGTGRTDVVMFRQGTGDYEDPSTFISNLYDD 403

QY 396 IFKI-----ISLARVAMQPFVGYSIYPRHLVSRAREFPFTTLTFLYEVNSSGYSQTTESV 449
Db 404 IYKLDLRAAAVSTIQAMDITFG-----VSSSRFPDIRGNQLYQSNKPYPSLPTIT 456

QY 450 LPIKINKDLPPSRNTNYSHRLSNAACVQNETSRV-----NVFGWTHTSMKKDNRIYDPKI 502
Db 457 FPG-ESSSEGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDNRNTILPDEI 515

QY 503 TQIPAVKAFALPAGTGYAGGYVTAGPYTGDDVVTLPYQA--SLKIRLTSAPTNNKRYVR 560
Db 516 TQIPAVTAYELRGNSS-----VVAGPGSTGGLVVKMSYHSVWSPFKVYCSL---KNYRVR 567

QY 561 LRYASGPGPFVRVERWSPSSVNSVNSANFSRPATGG-----YSSFDYVDTLVTFNOSGVE 613
Db 568 IRYASHGNCQFLMKRWPSTGVARHNRVVOGTFSNSMRYEAFKYLDITFTITPEENFA 627

QY 614 IIIQNLSGYHLIVDKVEFIPIDIQIEKCTKCFEGDICRCGVSQSLTKKEIVNSLFIN 672
Db 628 FTIDLESQGLDFIDKIEFIPV-----SGSAFYEYEGKQNIKTKQAVNDLFIN 674

RESULT 9
US-10-782-096-21
; Sequence 21, Application US/10782096
; Publication No. US20040210964A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
```

; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274148
; CURRENT APPLICATION NUMBER: US/10/782,096
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,633
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-096-21

Query Match 25.8%; Score 918.5; DB 4; Length 674;
Best Local Similarity 33.2%; Pred. No. 1.8e-71;
Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;

QY 4 MNSYQNTNEYEYLDGSPNNTNMSNRYPPAKDNPFPIN-----LDACQGRPWQDTWESV 57
DB 1 MNQYQNKNEYEYLESSQNNMNPYPFADDPNVMKNGYKDWNECEG-----SNISP 55

QY 58 SDIVTIGTYLIQFLPEPGIGGIPVIFSIINKLIPSSG-----QSVAAISICDLVSIIR 110
DB 56 SPAAATSKIIVSIVLTKLAKA--VASSLADSIKSSLGISKTITENNVSQVSMVQVHQIIN 113

QY 111 KEVDESIVLSDGVADPEGETAYQDYLYHYLEDWLTDKSNPKKLADVVKQFQAREEDFTKL 170
DB 114 RRIQETILDGESSLGLVAINRDYLGALAEANNKNSINQTNVAEAFKTVREFFFTK 173

QY 171 LAGSLRQKAEILLPTVYQAAHVLLLRDVAVKYKKEWGLVCPPLYPGSGRTDCHERLK 230
DB 174 LKGIYRTSSQITLLPTFTAANLHLSMLRDVAMYQEGWNL-----QSHINYSKELD 225

QY 231 AKIKEYTNCVGVWYKGLDQIROAGTSAEWSKFNKFRREMTLAVLDIIAIPPTDYFEKY 290
DB 236 DALEDYTNVCVEYTKGLNALR--GSTAIDWLEFNSFRDMTLVLDLVAIFPNVPVRY 283

QY 291 PLATSVELTREIYTPDVGYSYG--NYG-W----ERFFSFSNSVEANGTRGPGVLTWLAQIDI 344
DB 284 PLSTKISLSRKIYTPDVGRTDPSFGDWTNTGRTLANFNDLREVTDSPLVKWLGDMTI 343

QY 345 YSHSINLQGLYLSG-----WGTRHYEDFTKNGAFQMSGTTNNPRNIIIFGN---TD 395
DB 344 YTGAIIDSRYRPTSPGDRIGVWYGNINAFYHTGRTDVVMFRQTGDTAYEDPSTFISNLYDD 403

QY 396 IFKI-----ISLARYAMQPFVGYSTPRHLVSRAEFFPTTLNTFLYEVNSSGYSTIESV 449
DB 404 IYKDLRAAAVSTIQAMDITTFG-----VSSSRFFDIRGNQLYQSNKPYPSLPITIT 456

QY 450 LFGINKDLPPSTNTSHRLSNAACVQNETSRV-----NVFGWTHSTMKKNRIYPDKI 502
DB 457 FFG--EESSEGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDNRNTILPDEI 515

QY 503 TOIPAVKAPALPAGTYAGGYTAGGYTGCGDVTLPYQA--SLKIRLTSAPTNNKYRVR 560
DB 516 TOIPAVTAYELRGNSS-----VVAGPGSTGGDLVKMSYHVSFVKYCSL---KNYRVR 567

QY 561 LRYASGCGPPRVERWSPSSVSNANFSRPATG-----YSSFDVYDVLVTFNQSGVE 613
DB 568 IRYASHGNCQFLMKRWPFSTGVAPROWARNVQGTFSNSMRYEAFKYLIDITITPEENFPA 627

QY 614 IIQNLGSLGYHLIVDKVEFIPIDIQIEKCTKCPQEGDICRCEGVQSLETKEIIVNSLFIN 672
DB 628 FTIDLESGGDLFIDKIEFIPV-----SGSAFEYEGKQNIETKQKAVNDLFIN 674

RESULT 10
US-10-782-570-17
; Sequence 17, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-17

Query Match 25.8%; Score 918.5; DB 4; Length 674;
Best Local Similarity 33.2%; Pred. No. 1.8e-71;
Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;

QY 4 MNSYQNTNEYEYLDGSPNNTNMSNRYPPAKDNPFPIN-----LDACQGRPWQDTWESV 57
DB 1 MNQYQNKNEYEYLESSQNNMNPYPFADDPNVMKNGYKDWNECEG-----SNISP 55

QY 58 SDIVTIGTYLIQFLPEPGIGGIPVIFSIINKLIPSSG-----QSVAAISICDLVSIIR 110
DB 56 SPAAATSKIIVSIVLTKLAKA--VASSLADSIKSSLGISKTITENNVSQVSMVQVHQIIN 113

QY 111 KEVDESIVLSDGVADPEGETAYQDYLYHYLEDWLTDKSNPKKLADVVKQFQAREEDFTKL 170
DB 114 RRIQETILDGESSLGLVAINRDYLGALAEANNKNSINQTNVAEAFKTVREFFFTK 173

QY 171 LAGSLRQKAEILLPTVYQAAHVLLLRDVAVKYKKEWGLVCPPLYPGSGRTDCHERLK 230
DB 174 LKGIYRTSSQITLLPTFTAANLHLSMLRDVAMYQEGWNL-----QSHINYSKELD 225

QY 231 AKIKEYTNCVGVWYKGLDQIROAGTSAEWSKFNKFRREMTLAVLDIIAIPPTDYFEKY 290
DB 226 DALEDYTNVCVEYTKGLNALR--GSTAIDWLEFNSFRDMTLVLDLVAIFPNVPVRY 283

QY 291 PLATSVELTREIYTPDVGYSYG--NYG-W----ERFFSFSNSVEANGTRGPGVLTWLAQIDI 344
DB 284 PLSTKISLSRKIYTPDVGRTDPSFGDWTNTGRTLANFNDLREVTDSPLVKWLGDMTI 343

QY 345 YSHSINLQGLYLSG-----WGTRHYEDFTKNGAFQMSGTTNNPRNIIIFGN---TD 395
DB 344 YTGAIIDSRYRPTSPGDRIGVWYGNINAFYHTGRTDVVMFRQTGDTAYEDPSTFISNLYDD 403

QY 396 IFKI-----ISLARYAMQPFVGYSTPRHLVSRAEFFPTTLNTFLYEVNSSGYSTIESV 449
DB 404 IYKDLRAAAVSTIQAMDITTFG-----VSSSRFFDIRGNQLYQSNKPYPSLPITIT 456

QY 450 LFGINKDLPPSTNTSHRLSNAACVQNETSRV-----NVFGWTHSTMKKNRIYPDKI 502
DB 457 FFG--EESSEGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDNRNTILPDEI 515

QY 503 TOIPAVKAPALPAGTYAGGYTAGGYTGCGDVTLPYQA--SLKIRLTSAPTNNKYRVR 560
DB 516 TOIPAVTAYELRGNSS-----VVAGPGSTGGDLVKMSYHVSFVKYCSL---KNYRVR 567

QY 561 LRYASGCGPPRVERWSPSSVSNANFSRPATG-----YSSFDVYDVLVTFNQSGVE 613
DB 568 IRYASHGNCQFLMKRWPFSTGVAPROWARNVQGTFSNSMRYEAFKYLIDITITPEENFPA 627

QY 614 IIQNLGSLGYHLIVDKVEFIPIDIQIEKCTKCPQEGDICRCEGVQSLETKEIIVNSLFIN 672
DB 628 FTIDLESGGDLFIDKIEFIPV-----SGSAFEYEGKQNIETKQKAVNDLFIN 674


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RESULT 11
US-10-783-417-15
; Sequence 15, Application US/10783417
; Publication No. US20040216186A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274146
; CURRENT APPLICATION NUMBER: US/10/783,417
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,806
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-783-417-15

Query Match      25.8%; Score 918.5; DB 5; Length 674;
Best Local Similarity 33.2%; Pred. No. 1.8e-71;
Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;

QY      4 MNSYQNTNEYELDGSPNNNTNSNRYPPFAKDPNIFPIN-----LDACQGRPWQDTWESV 57
Db      1 MNQYQNKNEYEILESSQNNMNNPNRYPPADDPNAVKNMGNYKDWNECEG-----SNISP 55

QY      58 SDIVITGYLIQFLPEPGIGGIPVIFSINKLIPSSG-----QSVAAALSICDLVSIIR 110
Db      56 SPAAAITSKIVSVLTKLAKA--VASSLADSIKSSLSGISKITITENNVSQVSMVQVHQIIN 113

QY      111 KEVDESVLSDGVADPEGEMTAYQDYVLYHVLDELMTDKSNPKKLADVVKQFQAREDEFTKL 170
Db      114 RRIQETIIDLGGSSNLGLVAIYNRDYLGALEANNKNSNINQTNVAAEFKTVREFFTK 173

QY      171 LAGSLSRQKAEIILLPTVYQAAVHLLLRDVKYKKEWGLVCPPLYPGSGRTDCNERLK 230
Db      174 LKGIYRTSSQITLPTTQAAVHLLSRDLAVMYQEGWNL-----QSHINYSKELD 225

QY      231 AKIKEYTNYCVGWYKGLDQIRQAGTSAEVSFKFNKFRREMTLAVLDIIAIFPTDYDEKY 290
Db      226 DALEDYTNVCVEYTKGLNALR--GSTAIDWLEFNSFRDMLVLDLVAIFPNYNPVRY 283

QY      291 PLATSVELTRETITDPVGYSGG--NYG-W-----ERPFNSVEANGTRGRLVTLWQAI 344
Db      284 PLSTKISLSRKIYTDVPGRTDSPSGDWTNTGRTLANFNDLREVTDSPSLVKWLGDMTI 343

QY      345 YSHSINLQGLVLSG-----WGTTHRYEDFTKNGAFQMSGTTSNNPNIIFGN---TD 395
Db      344 YTGALDSYRPTSPGDRIGWYGNINAFYHTGRTDVVMFRQGTAYEDPSTFISNILDYD 403

QY      396 IFKI-----ISLARYAMQPFVGYGIPRHLVSRABEFPPTLNTFLYEVNSSGYSQTIESV 449
Db      404 IYKLDLRAAAVSTIQGAMDTTFG-----VSSSRFFDIRGNQLYQSNKPYPSLPITIT 456

QY      450 LPGAINKLPPSRNTYSHRLSNACVQNETSRV-----NVFGWTHSMKKDNRIYPDKI 502
Db      457 PFG--EESSEGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDNRNNTILPDEI 515

QY      503 TOIPAVKAFALPAGTYAGGYVYTAGPGYTGDDVTLPYQA--SLKIRLTSAPTNNKYRVR 560
Db      516 TOIPAVTAYELRGNS-----VVAGPGSTGGDLVVKMSYHSVWSFKVYSEL---KNYRVR 567

QY      561 LRYASGGPGPRFVERWSPSSVSNANFSPATCG-----YSSFDYVDTLVTTFNQSGVE 613
Db      568 IRYASHGNCQFLMKWEPSTGVAPROWARHNVQGTFSNSNRYEAFKYLDTFTTPENNPFA 627
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QY      614 IITQNLSGYHLIVDKVEFIPIDIQIEKTRCQCEGDCRCQEGVQSLETKKEIVNSLFIN 672
Db      628 FTIDLESGGDLFDKIEFIPV-----SGSAFEYEGKQNIETQKAVNDLFIN 674

RESULT 12
US-10-781-979-22
; Sequence 22, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-781-979-22

Query Match      25.8%; Score 918.5; DB 5; Length 674;
Best Local Similarity 33.2%; Pred. No. 1.8e-71;
Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;

QY      4 MNSYQNTNEYELDGSPNNNTNSNRYPPFAKDPNIFPIN-----LDACQGRPWQDTWESV 57
Db      1 MNQYQNKNEYEILESSQNNMNNPNRYPPADDPNAVKNMGNYKDWNECEG-----SNISP 55

QY      58 SDIVITGYLIQFLPEPGIGGIPVIFSINKLIPSSG-----QSVAAALSICDLVSIIR 110
Db      56 SPAAAITSKIVSVLTKLAKA--VASSLADSIKSSLSGISKITITENNVSQVSMVQVHQIIN 113

QY      111 KEVDESVLSDGVADPEGEMTAYQDYVLYHVLDELMTDKSNPKKLADVVKQFQAREDEFTKL 170
Db      114 RRIQETIIDLGGSSNLGLVAIYNRDYLGALEANNKNSNINQTNVAAEFKTVREFFTK 173

QY      171 LAGSLSRQKAEIILLPTVYQAAVHLLLRDVKYKKEWGLVCPPLYPGSGRTDCNERLK 230
Db      174 LKGIYRTSSQITLPTTQAAVHLLSRDLAVMYQEGWNL-----QSHINYSKELD 225

QY      231 AKIKEYTNYCVGWYKGLDQIRQAGTSAEVSFKFNKFRREMTLAVLDIIAIFPTDYDEKY 290
Db      226 DALEDYTNVCVEYTKGLNALR--GSTAIDWLEFNSFRDMLVLDLVAIFPNYNPVRY 283

QY      291 PLATSVELTRETITDPVGYSGG--NYG-W-----ERPFNSVEANGTRGRLVTLWQAI 344
Db      284 PLSTKISLSRKIYTDVPGRTDSPSGDWTNTGRTLANFNDLREVTDSPSLVKWLGDMTI 343

QY      345 YSHSINLQGLVLSG-----WGTTHRYEDFTKNGAFQMSGTTSNNPNIIFGN---TD 395
Db      344 YTGALDSYRPTSPGDRIGWYGNINAFYHTGRTDVVMFRQGTAYEDPSTFISNILDYD 403

QY      396 IFKI-----ISLARYAMQPFVGYGIPRHLVSRABEFPPTLNTFLYEVNSSGYSQTIESV 449
Db      404 IYKLDLRAAAVSTIQGAMDTTFG-----VSSSRFFDIRGNQLYQSNKPYPSLPITIT 456

QY      450 LPGAINKLPPSRNTYSHRLSNACVQNETSRV-----NVFGWTHSMKKDNRIYPDKI 502
Db      457 PFG--EESSEGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDNRNNTILPDEI 515

QY      503 TOIPAVKAFALPAGTYAGGYVYTAGPGYTGDDVTLPYQA--SLKIRLTSAPTNNKYRVR 560
Db      516 TOIPAVTAYELRGNS-----VVAGPGSTGGDLVVKMSYHSVWSFKVYSEL---KNYRVR 567
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2005, 09:48:35 ; Search time 197 Seconds
(without alignments)
1498.795 Million cell updates/sec

Title: US-10-782-141-3
Perfect score: 3556
Sequence: 1 MKNMNSYQNTNEYILDGSP.....CEGVQSLTKKKEIVNSLFIN 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3556	100.0	672	ADR89415	Adr89415 AXMI-008.
2	3540	99.6	669	ADR89417	Adr89417 AXMI-008
3	1872	52.6	666	ADR89439	Adr89439 cry40Aa1.
4	1571.5	44.2	693	ADR89402	Adr89402 AXMI-008.
5	1561.5	43.9	690	ADR89404	Adr89404 AXMI-008.
6	918.5	25.8	674	ADR89435	Adr89435 cry24Aa.
7	833.5	23.4	682	ADR89408	Adr89408 AXMI-009.
8	801.5	22.5	1151	9 ABA81457	Aea81457 Bacillus
9	801.5	22.5	1156	2 AAW46856	Aaw46856 Bacillus
10	801.5	22.5	1156	2 AAV24959	Aay24959 Bacillus
11	801.5	22.5	1156	3 AEA81456	Aea81456 Bacillus
12	801.5	22.5	1279	3 AAY82988	Aay82988 Native Cr
13	789.5	22.2	652	3 AAY83039	Aay83039 Cry9Aa to
14	787	22.1	656	3 AAY83040	Aay83040 Synthesis
15	782.5	22.0	671	8 ADR89410	Adr89410 AXMI-009
16	776.5	21.8	1210	5 AAU99256	Aau99256 Bacillus
17	776.5	21.8	1210	8 ADL15307	Adl15307 B thuring
18	776.5	21.8	1210	9 AEB45609	Aeb45609 B. thuring
19	776	21.8	1157	2 AAR27343	Aar27343 B. thuring
20	776	21.8	1157	2 AAR44208	Aar44208 Bacillus
21	773.5	21.8	1230	8 ADK98484	Adk98484 B thuring
22	773.5	21.8	1230	8 ADK98489	Adk98489 B thuring
23	773.5	21.8	1230	8 ADK98481	Adk98481 B thuring
24	773.5	21.8	1230	8 ADK98491	Adk98491 B thuring

25	773.5	21.8	1230	8	ADK98487	Adk98487 B thuring
26	773	21.7	1157	2	AAR28900	Aar28900 Toxin 50C
27	773	21.7	1157	2	AAR25997	Aar25997 Delta-end
28	773	21.7	1157	2	AAR33768	Aar33768 Bt isolat
29	773	21.7	1157	2	AAW06418	Aaw06418 Antiscara
30	773	21.7	1157	8	ADR89430	Adr89430 cry8Aa. 1
31	773	21.7	1157	9	ADY59865	Ady59865 Bacillus
32	772.5	21.7	1229	2	AAR54074	Aar54074 CryET5. 2
33	772.5	21.7	1229	2	AAW35259	Aaw35259 Bacillus
34	772.5	21.7	1229	2	AAW17699	Aaw17699 CryET5. 3
35	772.5	21.7	1229	2	AAW87633	Aaw87633 CryET5 pr
36	772.5	21.7	1229	2	AAW30923	Aaw30923 B. thuring
37	772.5	21.7	1229	8	ADK98479	Adk98479 B thuring
38	770.5	21.7	802	4	AAU02035	Aau02035 B. thurin
39	765.5	21.5	661	8	ADR89412	Adr89412 AXMI-009
40	765	21.5	1167	5	AAB02081	Aab02081 Bacillus
41	756.5	21.3	719	3	ABH07073	Abh07073 Bacillus
42	756.5	21.3	719	9	ADY59880	Ady59880 Bacillus
43	756.5	21.3	719	9	ADY59881	Ady59881 Bacillus
44	756	21.3	1209	4	AAU02094	Aau02094 Bacillus
45	756	21.3	1228	9	ADY59858	Ady59858 Bacillus

ALIGNMENTS

RESULT 1		
ADR89415		
ID	ADR89415 standard; protein; 672 AA.	
XX	AC	ADR89415;
XX	DT	18-NOV-2004 (first entry)
XX	DE	AXMI-008.
XX	KW	delta-endotoxin; delta-endotoxin associate polypeptide;
KW	expression cassette; transformation; transgenic; plant;	bacteria;
KW	lepidoptera; coleoptera; pest; pesticide; resistance;	pesticidal activity.
XX	OS	Bacillus thuringiensis.
XX	FH	Key
FT	Misc-difference 1	Location/Qualifiers
FT	/note= "Encoded by GTG"	
XX	PN	WO2004074462-A2.
XX	PD	02-SEP-2004.
XX	PF	20-FEB-2004; 2004WO-US005829.
XX	PR	20-FEB-2003; 2003US-0448632P.
PR	20-FEB-2003; 2003US-0448633P.	
PR	20-FEB-2003; 2003US-0448797P.	
PR	20-FEB-2003; 2003US-0448806P.	
PR	20-FEB-2003; 2003US-0448810P.	
PR	20-FEB-2003; 2003US-0448812P.	
PR	19-FEB-2004; 2004US-00781979.	
PR	19-FEB-2004; 2004US-00782020.	
PR	19-FEB-2004; 2004US-00782096.	
PR	19-FEB-2004; 2004US-00782141.	
PR	19-FEB-2004; 2004US-00782570.	
PR	19-FEB-2004; 2004US-00783417.	
XX	(ATHE-) ATHENIX CORP.	
XX	Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;	
XX	WPI: 2004-635574/61.	
XX	N-PSDB; ADR89413, ADR89414.	

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.

XX
PS Claim 12; SEQ ID NO 27; 178pp; English.

XX This sequence represents an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.

XX
SQ Sequence 672 AA;

Query Match 100.0%; Score 3556; DB 8; Length 672;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKNMNSYQNTNEYEILDGSPNNTMNSNRYFPAKDPNIPINLDACQGRPWQWTSVSDI 60
Db 1 MKNMNSYQNTNEYEILDGSPNNTMNSNRYFPAKDPNIPINLDACQGRPWQWTSVSDI 60
Qy 61 VTIGTYLIQFLLEPGIGGIPVIFSIINKLI PSSGQSVAAALSCDILVSIIRKEVDSVLS 120
Db 61 VTIGTYLIQFLLEPGIGGIPVIFSIINKLI PSSGQSVAAALSCDILVSIIRKEVDSVLS 120
Qy 121 GVADPEGEMTAYQDYLYLHLEDWLTDSKPKLADVVKQFOAREDEFTKL LAGSLSRKA 180
Db 121 GVADPEGEMTAYQDYLYLHLEDWLTDSKPKLADVVKQFOAREDEFTKL LAGSLSRKA 180
Qy 181 EILLPTVYQANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLKAKEYTNYC 240
Db 181 EILLPTVYQANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERLKAKEYTNYC 240
Qy 241 VGWYKGLDQIQAQTSAEVSKFNKFRREMTLAVLDIIAIPPTVDFEYPIATSVELTR 300
Db 241 VGWYKGLDQIQAQTSAEVSKFNKFRREMTLAVLDIIAIPPTVDFEYPIATSVELTR 300
Qy 301 EIYTDVPVGYSGNYGWERFFSNFVSVEANGTRGPGVLTWLQADIIYSHSINLQGLSGWG 360
Db 301 EIYTDVPVGYSGNYGWERFFSNFVSVEANGTRGPGVLTWLQADIIYSHSINLQGLSGWG 360
Qy 361 GTRHYEDFTKGNAGFORMSGTTSNNPNIIFGNTDIFKIIISLARYAMOPFVGYSIPRHV 420
Db 361 GTRHYEDFTKGNAGFORMSGTTSNNPNIIFGNTDIFKIIISLARYAMOPFVGYSIPRHV 420
Qy 421 SRAEFFPTLNTFLYEVNSSGYSTIESVLPKINKDLPSPRTNYSHRLSNAACVQNETSR 480
Db 421 SRAEFFPTLNTFLYEVNSSGYSTIESVLPKINKDLPSPRTNYSHRLSNAACVQNETSR 480
Qy 481 VNVGWTHTSMKDNRIYDPDKITQIPAVKAFALPAGTGYAGGYVTAGPGYTGDDVTLPI 540
Db 481 VNVGWTHTSMKDNRIYDPDKITQIPAVKAFALPAGTGYAGGYVTAGPGYTGDDVTLPI 540
Qy 541 QASLKIRLTSAPTNNKYRVLRYASGGPGPFVERWSPSSVSNANFSPATGYSFSDVY 600
Db 541 QASLKIRLTSAPTNNKYRVLRYASGGPGPFVERWSPSSVSNANFSPATGYSFSDVY 600
Qy 601 DTLVTFNQSGVEIIIQNLGSHYLLVDKVEFIPIDIQIEKTKCFEGDICRCEGVQSL 660
Db 601 DTLVTFNQSGVEIIIQNLGSHYLLVDKVEFIPIDIQIEKTKCFEGDICRCEGVQSL 660
Qy 661 TKKEIVNSLFIN 672
|||||

Db 661 TKKEIVNSLFIN 672

RESULT 2

ADR89417
ID ADR89417 standard; protein; 669 AA.

XX ADR89417;

DT 18-NOV-2004 (first entry)

DE AXMI-008 alternative protein.

KW delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.

OS Bacillus thuringiensis.

XX WO2004074462-A2.

XX 02-SEP-2004.

XX 20-FEB-2004; 2004WO-US005829.

XX 20-FEB-2003; 2003US-0448632P.

XX 20-FEB-2003; 2003US-0448633P.

XX 20-FEB-2003; 2003US-0448797P.

XX 20-FEB-2003; 2003US-0448806P.

XX 20-FEB-2003; 2003US-0448810P.

XX 20-FEB-2003; 2003US-0448812P.

XX 19-FEB-2004; 2004US-00781979.

XX 19-FEB-2004; 2004US-00782020.

XX 19-FEB-2004; 2004US-00782141.

XX 19-FEB-2004; 2004US-00782570.

XX 19-FEB-2004; 2004US-00783417.

XX (ATHE-) ATHENIX CORP.

XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

XX WPI; 2004-635574/61.

XX N-PSDB; ADR89416.

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.

PS Claim 12; SEQ ID NO 29; 178pp; English.

XX This sequence represents an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.

XX SQ Sequence 669 AA;

Query Match 99.6%; Score 3540; DB 8; Length 669;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 MNSYQNTNEYEILDGSPNNNTNNSNRYPPAKDPNIPINLDACQGRPMQDTWESVSDIVTI 63
Db 1 MNSYQNTNEYEILDGSPNNNTNNSNRYPPAKDPNIPINLDACQGRPMQDTWESVSDIVTI 60
QY 64 GTYLQFLLEPGIGGIPVIFSINKLIPSSGOSVAALSICDLVSIIRKEVDESLSGVA 123
Db 61 GTYLQFLLEPGIGGIPVIFSINKLIPSSGOSVAALSICDLVSIIRKEVDESLSGVA 120
QY 124 DFEGMTAYQDYLLHYLEDWLTDKSNPKKLADVVQFOQAREEDFTKLAGSLSRQKAEIL 183
Db 121 DFEGMTAYQDYLLHYLEDWLTDKSNPKKLADVVQFOQAREEDFTKLAGSLSRQKAEIL 180
QY 184 LLPTVVOAANVHLLLRDVAVKYKKEWGLVCPPLYPGSGRTDCNERLKAKEITYNCVGM 243
Db 181 LLPTVVOAANVHLLLRDVAVKYKKEWGLVCPPLYPGSGRTDCNERLKAKEITYNCVGM 240
QY 244 YNKGDDQIRQAGTSAEVNSKFNKFRREMTLAVLDIIAIPPTDYDFEKYPLATSVELTREY 303
Db 241 YNKGDDQIRQAGTSAEVNSKFNKFRREMTLAVLDIIAIPPTDYDFEKYPLATSVELTREY 300
QY 304 TDPVGYSGNYGWERFFSGFNSVEANGTRGPGGLVTLQADIIYSHSINLQGLYSGWGTR 363
Db 301 TDPVGYSGNYGWERFFSGFNSVEANGTRGPGGLVTLQADIIYSHSINLQGLYSGWGTR 360
QY 364 HYEDFTKNGAFORMSGTSSNNPRNIIFGNTDIFKIISLARYAMQPFVGYISIPRHLVSR 423
Db 361 HYEDFTKNGAFORMSGTSSNNPRNIIFGNTDIFKIISLARYAMQPFVGYISIPRHLVSR 420
QY 424 EFPFTLTATFLYEVNSSGYSTIESVLPQINKDLPPSRNTYSHRLSNAACVQNETSRNV 483
Db 421 EFPFTLTATFLYEVNSSGYSTIESVLPQINKDLPPSRNTYSHRLSNAACVQNETSRNV 480
QY 484 FGWHTSMKKDNRIYDPDKITQIPAVKAFALPAGTGAGGYVTAGPYTGDDVVTLPYQAS 543
Db 481 FGWHTSMKKDNRIYDPDKITQIPAVKAFALPAGTGAGGYVTAGPYTGDDVVTLPYQAS 540
QY 544 LKIRLTSAPTNNKYRVLRYASGGPGPRVERWSPSSVSNANFSPATGGYSSFDYVDTL 603
Db 541 LKIRLTSAPTNNKYRVLRYASGGPGPRVERWSPSSVSNANFSPATGGYSSFDYVDTL 600
QY 604 VTTNQSQVEIIQNLSGYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCEGVQSLETKK 663
Db 601 VTTNQSQVEIIQNLSGYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCEGVQSLETKK 660
QY 664 EIVNSLFIN 672
Db 661 EIVNSLFIN 669
RESULT 3
ADR89439
ID ADR89439 standard; protein; 666 AA.
XX AC
XX ADR89439;
XX DT
XX 18-NOV-2004 (first entry)
XX DE cry40aa1.
XX KW delta-endotoxin; delta-endotoxin associate polypeptide;
XX KW expression cassette; transformation; transgenic; plant; bacteria;
XX KW lepidoptera; coleoptera; pest; pesticide; resistance;
XX KW pesticidal activity.
XX OS
XX Bacillus thuringiensis.
XX EN WO2004074462-A2.
XX FD
XX 02-SEP-2004.
XX PF
XX 20-FEB-2004; 2004WO-US005829.
XX XX
XX 20-FEB-2003; 2003US-0448632P.
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PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
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(ATHE-) ATHENIX CORP.

Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

WPI; 2004-635574/61.

New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.

Example 6; SEQ ID NO 51; 178pp; English.

This sequence represents a delta-endotoxin crystal protein. This protein was included in the scope of the invention as a comparison to the delta-endotoxins of the invention. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

Sequence 666 AA;

Query Match 52.6%; Score 1872; DB 8; Length 666;

Best Local Similarity 57.0%; Pred. NO. 1.3e-165;

Matches 392; Conservative 91; Mismatches 161; Indels 44; Gaps 15;

QY 5 NSYQNTNEYEILDGSPNNNTNNSNRYPPAKDPNIPINLDACQGRPMQDTWESVSDIVTI 64

Db 1 NSYENKNEVEILLESSNNTNMPNRYPPANDRDMSTMSFNDCCQGISWDEIWESAEITISIG 60

QY 65 TYLIQFLLEPGIGGIPVIFSINKLIPSSGOSVAALSICDLVSIIRKEVDESLSGVA 124

Db 61 IDLIEFLMEPSLGGINTLFSIIGKLIPTNHSQSALSICDLLSIRKEVADSLSDAICR 120

QY 125 F-EGEMTAYQDYLLHYLEDWLT-----KSNPKKLADVVQFOQAREEDFTKLAGSLSRQ 178

Db 121 FLDDGKLKNRYEYLPLEAWLKDGPLOKTNNSDGLQVLYFELSFRDNEILGGSLARN 180

QY 179 KAEILLLPTVVOAANVHLLLRDVAVKYKKEW-----GLVCPPLYPGSG---RTDCNER 228

Db 181 NQAILLLPYFCASCKQLLLLDADAQVYEQWPFPLSAENVRSSELISPSNGCDFTGYDER 240

QY 229 LKAKIKEITYNCVGNKGLDQIRQAGTSAEVNSKFNKFRREMTLAVLDIIAIPPTDYFE 288

Db 241 LKCKIAEVTDYCEYVQAGLNQIKOAGTGADTWAKFNKFRREMTLAVLDIIAIFQYDFK 300

QY 289 KYPLATSVELTREIYTDVPGYSGNYGWERFF--SFNSVEANGTRGPGGLVTLWLOAIDYS 346

Db 301 KYPLPTHVELTREIYTDVPGYSSGYTSMWKYTGAFNTLEANGTRGPGGLVTLWLSIGYN 360

QY 347 HSNILQLGVLSCWGGTRHYEDFTKNGAFORMSGTSSNNPRNIIFGNTDIFKIISLARYA 406

Db 361 EYVS---RYFGWVGTRHYEDYTTNGNFGNFORMSGTTSDRLDISFPNSDIFKIES---KA 414
 Qy 407 MQPFGV--YSIPRHLVSRABEFTTLNTEFLVNSGY-SQTIESVLGINKDLPPSRTN 463
 Db 415 IMNLVGEINARPEYRVSRABEFTTLYLDAGNSGLSSMTITTSKLFQI-KNPEPSYRD 473
 Qy 464 YSHRLSNAACVQNETSRVNVFGWTHSMKKDNRIYDPDKITQIPAVKAFALPAGTCVAGGY 523
 Db 474 YSHRLSNAACVAGNSRNLVNGWTHSMKYNLIYDPDKITQIPAVKAFEDI-SDTG--PQ 530
 Qy 524 VTAGPGYTGDDVTLTPYQASLKIRLTSAPTNKNVRLRYASGGPGPRVERWSPSSVSN 583
 Db 531 VIAGPGHTGGNVSLPYYSRLKIRLIPASTNKNVLRVRYTSTNGRLLVERWSPSSIIN 590
 Qy 584 ANFSRATGYSYSDYDVTLTFTNQSGVEIIQNLGSHLIVDKVEFIPIDIQIEKCTK 643
 Db 591 SYFELPSTGPGDSFGYDVTLTFTNQSGVEIIQNLDPINVDKVEFIPVN-----STA 644
 Qy 644 QFEGDICRCGVSQSLKTKKIVNSLFI 671
 Db 645 LEYEGK-----OSLEKAQDVNDLFV 665

RESULT 4

AD89402

ID AD89402 standard; protein; 693 AA.

XX AC AD89402;

DT 18-NOV-2004 (first entry)

XX DE AXMI-008.

KW delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; plant; bacteria;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.

XX OS Bacillus thuringiensis.

XX FH Location/Qualifiers

FT Misc-difference 1 /note= "Encoded by GTG"

FN WO2004074462-A2.

XX PD 02-SEP-2004.

XX PF 20-FEB-2004; 2004WO-US005829.

XX PR 20-FEB-2003; 2003US-0448632P.

XX PR 20-FEB-2003; 2003US-0448633P.

XX PR 20-FEB-2003; 2003US-0448797P.

XX PR 20-FEB-2003; 2003US-0448806P.

XX PR 20-FEB-2003; 2003US-0448810P.

XX PR 19-FEB-2004; 2004US-00781979.

XX PR 19-FEB-2004; 2004US-00782020.

XX PR 19-FEB-2004; 2004US-00782036.

XX PR 19-FEB-2004; 2004US-00782141.

XX PR 19-FEB-2004; 2004US-00782570.

XX PR 19-FEB-2004; 2004US-00783417.

XX PA (ATHE-) ATHENIX CORP.

XX PI Carozzi N, Hargiss T, Kozziel MG, Duck NB, Carr B;

XX DR WPI; 2004-635574/61.

XX DR N-PSDB; AD89400, AD89401.

XX

PS Claim 12; SEQ ID NO 14; 178pp; English.

CC This sequence represents an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.

XX Sequence 693 AA;

Query Match 44.2%; Score 1571.5; DB 8; Length 693;

Best Local Similarity 47.2%; Pred. No. 2.1e-137;

Matches 340; Conservative 107; Mismatches 198; Indels 75; Gaps 18;

Qy 1 MKMNSYQNTNEYEILDGSPNNTNMSNRYPPAKDPIFPINLDACGRPWQWTWESVDI 60

Db 1 MKKMSFYQNKNEYEILESSNNNTNRYPPFANRDMSTMWNCQGISWDEIWESVETI 60

Qy 61 VTIGTYLQIFLPGGIGPVIIFSINKLIPSSGOSVAALSICDLVSIIRKEVDESVLSD 120

Db 61 TSGINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLVSIIRKEVADSVLSD 120

Qy 121 GVADFEGETAYQDYLLHYLEDWLT-----KSNPKKLADVVKVQFOAREDEFTKLGLSGL 175

Db 121 AIADPDGKLKNRYEYLSYLGAWLADGKPLQKTNSDGLQVYFKLSERDFNEILGSSL 180

Qy 176 SRQKAEIILLPTYQAAVHLLLDRAVYKKEW-----GLVCPPLYPGSG---RTDC 225

Db 181 SRNNAQVLLPTFAQAAVQLLLDRDAVQYKAWFPFLSAENVRSLSIPNSGCDFTGDY 240

Qy 226 NERLKAKIKEYTNYCVGWYKGLDQIRQAGTSAEYVSKENKFERREMTLAVLDIIAIFPTY 285

Db 241 YERLCKTAEYTNCLYWTQVGLNQIKGGTADTWSKFNKFRREMTLAVLDIIAIFPTY 300

Qy 286 DFEKYPLATSVELTREIYTDVPVYSGNGYGRERF---SFNSVEANGTRGPGVTLWQAID 343

Db 301 DFEKYPLTHVELTREIYTDVAGYSGTYSLRWNPNTFNGLEANGTRGPGVTLWLSKIG 360

Qy 344 IYSHSINILQGLYSGWGGTRHYEDFTKNGAFQRMSTNNPRNIIFGNTDIPKILSLA 403

Db 361 IYNEYVS---RYFAGWVGTRHYEDYTKNGIFQRMSTNNDLRNTDFQNAVYKITS- 416

Qy 404 RYAMQPFVGYSI--PRHLVSRAEFFPTTLNTEFLVNSSGYSQ-TTESVLP-----GIN 454

Db 417 --AIMNLVGETTARPEYRVSKADFRVGGPDLNLDAGNGLSRMTIESTFPLVLHNGVR 474

Qy 455 KDLPPSRNTNYSRLSNAACVQNETSRVNVFGWTHSMKKDNRIYDPKIQIPAVKAFALP 514

Db 475 -----GPSHRLSNAACVYGNRNVYGTHTSLKRENIIEANQIQIPAVKSYLQ 526

Qy 515 AGTYAGGYVTAGPGYTGDDVVT-----PYQA-----SLKIRLTSAPTNKNVRLRYA 564

Db 527 NYLANAYTVIKGT-HTGGDLIRFLRTKSEYNNAVAGGIGIRLIINNKTAGSQSYRIFRYA 585

Qy 565 SGGPGPFRVERWSPSSVSN--ANFSRATG-----YSSFDYDVTLTFTNQSGVLIIC 617

Db 586 ADKAAFFSVLYPGGWSNRFVSLKSYSGNVDLLKYSDFKFAEIIPTLPSSNIQMDVE 645

Qy 618 N-----LSGYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCGVSQSLKTKKIVNSLFIN 672

Db 646 MQANSFQSDVNVLDKIEFLP-----SNVTILEYEGE-----RDEKTKNAVNDLFTN 693

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.

RESULT 5

ADR89404
 ID ADR89404 standard; protein; 690 AA.
 XX AC ADR89404;
 XX DT 18-NOV-2004 (first entry)
 XX DE AXMI-008 alternative protein.
 XX KW delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; plant;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.
 XX OS Bacillus thuringiensis.
 XX PN WO2004074462-A2.
 XX PD 02-SEP-2004.
 XX PF 20-FEB-2004; 2004WO-US005829.
 XX PR 20-FEB-2003; 2003US-0448632P.
 PR 20-FEB-2003; 2003US-0448633P.
 PR 20-FEB-2003; 2003US-0448797P.
 PR 20-FEB-2003; 2003US-0448806P.
 PR 20-FEB-2003; 2003US-0448810P.
 PR 19-FEB-2003; 2003US-0448812P.
 PR 19-FEB-2004; 2004US-00781979.
 PR 19-FEB-2004; 2004US-00782020.
 PR 19-FEB-2004; 2004US-00782096.
 PR 19-FEB-2004; 2004US-00782141.
 PR 19-FEB-2004; 2004US-00782570.
 PR 19-FEB-2004; 2004US-00783417.
 XX PA (ATHE-) ATHENIX CORP.
 XX PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
 XX N-PSDB; ADR89403.
 DR WPI; 2004-635574/61.
 DR N-PSDB; ADR89403.
 XX PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.
 XX PS Claim 12; SEQ ID NO 16; 178pp; English.
 XX CC This sequence represents an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.
 XX SQ Sequence 690 AA;
 Query Match 43.9%; Score 1561.5; DB 8; Length 690;
 Best Local Similarity 47.1%; Pred. No. 1.8e-136;
 Matches 338; Conservative 107; Mismatches 197; Indels 75; Gaps 18;
 Qy 4 MNSYONTNEYELDGGSPNNNTNMSNRYPPAKDNPFPINLDACQGRPWQDTWESVDIVTI 63
 Db 1 MSPYQNKNEYELLESSNNNTNPNRYPPANNRDMSTMWNCQGISWDEIWSVETITSI 60

QY 64 GTYLIOFLLEPGIGGIPVIFSIINKLIPSSQSVAAALSICDLVSIIRKEVDSEVLSDGVA 123
 DB 61 GINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLLSIIRKEVADSVLSDAIA 120
 QY 124 DFEGMTAYQDYLYLHYLEDWLT-----KSNPKKLADVVKFOAREEDFTKLGLASLRQ 178
 DB 121 DFDGKLKNRYEYLYSLGAWLKDGPLOKNTNSDIGOLVYVYFKLSERDFNEILGSLSRN 180
 QY 179 KAEIILLPTVVOAANVHLLLRDAVKYKKEW-----GLVCPPLYPGSG---RTDCNER 228
 DB 181 NAQVLLLPFAAANVQLLLRDVAVQYKAQMPFELSAENVRSSELISPSNGCDFTGDYTER 240
 QY 229 LKAKIKEYTNYCVGWYKNGLDIQRQAGTSAEVSKFNKFRREMTLAVLDIIAIPPTYDFE 288
 DB 241 LKCKTAEYNYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLDIIAIPPTYDFE 300
 QY 289 KYPLATSVELTREIYTDVPGYSGNYGWERFF--SFNSVEANGTRGPGLVTLQALDIYS 346
 DB 301 KYPLPTHVELTREIYTDVAVGYSSGYTSMWRNWPNTFNGLEANGTRGPGLVTLWSKGIYN 360
 QY 347 HSINLQILGYLSHGGRHYEDFTKNGAFORMSGTTNNPNRIIFGNTDIFKILSLARYA 406
 DB 361 EYVS---RYFAGWVGTRHYEDYTKNGIFQFORMSGTTSDNLRNIDFNADVYKITSLS---A 414
 QY 407 MQPFVGYSI--PRHLVSRAEFFFTTLNTFLYEVNSSGYSQ--TIESVLP-----GINKDL 457
 DB 415 IMNLVGETTARPEYRVSKADFRVGGPDLDYDAGNGLSRMTIESTPPLVLHSGVR--- 471
 QY 458 PPSRTNYSRLSNAACVQNETSRVNVFGWTHSMKKDNRIYPDKITQIPAVKAFALPAGT 517
 DB 472 ----GPHRLSNAACVYGVNSRVNVYGWTHSLKRENIIEANGITQIPAVKSYLYQNYL 526
 QY 518 GYAGGYVTAGPGYTGDDVVTL-----PYQA-----SLKIRLTSAPTKNYRVRLRYASGG 567
 DB 527 ANAYTVIKGT-HTGGDLIRFLRTKSEYNVAVAGGGIRLIINNKTAGQSYRIRFYAADK 585
 QY 568 PGPFVRVERMSPSVSN--ANFSRPATGG-----YSPDYVDVTLVTTFNQSGVEIILQN-- 618
 DB 586 AAFPSVLYPGGWSNRFRVLSLEKSYSGNYDDLKYSDFKFAIITPPLPSSNIQMDVENQA 645
 QY 619 ---LSGVHLIVDKVERPIPIQIEKCTKQCEGICRCGVQSLTKKEIVNSLFIN 672
 DB 646 NSFQSDVNVVLDKIEFLP-----SNTTLEYEGE-----RDLEKTKNAVNDLFTN 690

RESULT 6

ADR89435
 ID ADR89435 standard; protein; 674 AA.
 XX AC ADR89435;
 XX DT 18-NOV-2004 (first entry)
 XX DE cry24Aa.
 XX KW delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; plant;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.
 XX OS Bacillus thuringiensis.
 XX PN WO2004074462-A2.
 XX PD 02-SEP-2004.
 XX PF 20-FEB-2004; 2004WO-US005829.
 XX PR 20-FEB-2003; 2003US-0448632P.
 PR 20-FEB-2003; 2003US-0448633P.
 PR 20-FEB-2003; 2003US-0448797P.
 PR 20-FEB-2003; 2003US-0448806P.


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PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX (ATHE-) ATHENIX CORP.
XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
XX and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX for producing organisms with pesticide resistance.
XX
XX Example 6; SEQ ID NO 47; 178pp; English.
XX
XX This sequence represents a delta-endotoxin crystal protein. This protein
XX was included in the scope of the invention as a comparison to the delta-
XX endotoxins of the invention. Some of the delta-endotoxin coding sequences
XX of the invention have alternative start codons, producing more than one
XX protein from a single open reading frame. The nucleic acid sequences of
XX the invention are useful in DNA constructs or expression cassettes for
XX transformation and expression in plants and bacteria. The nucleic acids
XX and corresponding polypeptides are useful for killing lepidopteran or
XX coleopteran pests. Compositions containing the delta-endotoxins of the
XX invention, and methods for their production, are useful for the
XX production of organisms with pesticide resistance, specifically bacteria
XX and plants. These organisms are useful for generating altered or improved
XX delta-endotoxin or delta-endotoxin-associated proteins that have
XX pesticidal activity, or for detecting the presence of delta-endotoxin or
XX delta-endotoxin-associated proteins or nucleic acids in products or
XX organisms.
XX
XX Sequence 674 AA;
XX
XX Query Match 25.8%; Score 918.5; DB 8; Length 674;
XX Best Local Similarity 33.2%; Pred. No. 3.5e-76;
XX Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;
XX
XX 4 MNSYQNTNEYILDGSPNNMNSRYPFAKDPNIPIN-----LDACQGRPMQDWESV 57
XX 1 MNQYQNKNEYILESSQNNMNPYPFADDDNAVMMKNGYKDWVNECEG-----SNIS 55
XX
XX 58 SDIVTIGTYLQFLPEGGIGGIPVIFSIINKLIPSG-----QSVAAISICDLVSIIR 110
XX 56 SPAAAITSKIIVSLVLTAKA--VASSLADSIKSLGISTKTITENNVSQVSVQVHQIIN 113
XX
XX 111 KEVDESVLSDGVADPEGETAYODYVLYHLEDLTDKSNPKKLADVVKQFOAREEDFTKL 170
XX 114 RRIQETILDGESSNLGLVAIYNRYDLGALNWNKNSINQTNVAEAFKVEREFFTKL 173
XX
XX 171 LAGSLRQKAEILLPTTYVQAAVNHLLLRDVAVKYKKEWGLVCPPLPGSGRTDCNERLK 230
XX 174 LKGIVRTSSQITLPTTFOAANHLMLRDVAVMYQEGWNL-----QSHINYSKELD 225
XX
XX 231 AKIKEYTYCVGWYKGLDQIRQAGTSARVWSKFNKFRREMTLAVLDIIAIFPTDYFKY 290
XX 226 DALEDYTYNCEVYTKGLNALR--GSTAIDWLEFNSFRDMDTLVLDLVAIFPNVPVRY 283
XX
XX 291 PLATSVELTREIYTDPPVGYSGG-NYG-W---ERPFNSVSEANGTRGPGLVTLWQAIDI 344
XX 284 PLUSTKISLSRKIYTDVGRGTDSPSGDWTNTGRTLANFNDLEREVDTSFLVNLGDMTI 343
XX
XX 345 YSHSINLQGLYLSG-----WGTREHYEDFTKNGAFQRMSTGTTNNPRNIIFGN---TD 395
XX 344 YTGAIYSRPTSPGRIGVWYGNINAFYHTGRTDVVMFQTGDTAYEDPSTFISNLYDD 403
XX 336 IFKI-----ISLARYAMQPFVGYSIPLHLVSRARFFPTTLNTFLYEVNSSGYSTIESV 449
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Db 404 IYKDLRAAAVSTIQGMDTTF-----VSSRFDIRGRNQLQSNKPFYSLPTIT 456
QY 450 LPGINKDLPSPRTNYSRLSNAACVQNETSRV-----NVFGWHTHTSMKKDNRIYDPDKI 502
Db 457 FPG-BESSEGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDNRNNTILPDEI 515
QY 503 TOIPAVKAFALPAGTGYAGGYTAGPGYTGDDVTLPYQA--SLKRLTTSAPTNNKRYVR 560
Db 516 TOIPAVTAYELRGNSS-----VVAGPGSTGGDLVKNYSYHVSFVKYCYSEL---KNRYVR 567
QY 561 LRYASGGPGPFRVERWSPSSVSNANFSRPAATG-----YSSFDVYVDLVTTFNOSGVE 613
Db 568 IRYASHGNCQFLMKRPSTGVAPQWARHNVQTFSNSMRYEAFKYLIDFTITPENNFA 627
QY 614 IIQMLSGVHLIVDKVEFIPIDIIQIEKTKCFEGDICRCEGVQSLETKEIVNSLFIN 672
Db 628 FTIDLESQGLDFIDKIEFIPV-----SGSAFEYEGKQNIETKQKAVNDLFIN 674
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RESULT 7

ADR89408

ID ADR89408 standard; protein; 682 AA.

XX AC ADR89408;

XX DT 18-NOV-2004 (first entry)

XX DE AXMI-009.

XX KW delta-endotoxin; delta-endotoxin associate polypeptide;

XX KW expression cassette; transformation; transgenic; plant; bacteria;

XX KW lepidoptera; coleoptera; pest; pesticide; resistance;

XX KW pesticidal activity.

XX OS Bacillus thuringiensis.

XX PN WO200407462-A2.

XX PD 02-SEP-2004.

XX PF 20-FEB-2004; 2004WO-US0005829.

XX PR 20-FEB-2003; 2003US-0448632P.

XX PR 20-FEB-2003; 2003US-0448633P.

XX PR 20-FEB-2003; 2003US-0448797P.

XX PR 20-FEB-2003; 2003US-0448806P.

XX PR 20-FEB-2003; 2003US-0448810P.

XX PR 20-FEB-2003; 2003US-0448812P.

XX PR 19-FEB-2004; 2004US-00781979.

XX PR 19-FEB-2004; 2004US-00782020.

XX PR 19-FEB-2004; 2004US-00782096.

XX PR 19-FEB-2004; 2004US-00782141.

XX PR 19-FEB-2004; 2004US-00782570.

XX PR 19-FEB-2004; 2004US-00783417.

XX (ATHE-) ATHENIX CORP.

XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

XX WPI; 2004-635574/61.

XX N-PSDB; ADR89407.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
XX and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX for producing organisms with pesticide resistance.

XX Claim 12; SEQ ID NO 20; 178pp; English.

XX This sequence represents an isolated delta-endotoxin. Some of the delta-
XX endotoxin coding sequences of the invention have alternative start
XX codons, producing more than one protein from a single open reading frame.
XX The nucleic acid sequences of the invention are useful in DNA constructs

or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

XX Sequence 682 AA;

Query Match 23.4%; Score 833.5; DB 8; Length 682;
Best Local Similarity 33.8%; Pred. No. 3.4e-68;
Matches 257; Conservative 112; Mismatches 222; Indels 169; Gaps 40;

QY 4 MNSYQNTNEYELDGSPPNNTMSN---RYPPAKDPNIFPINLDACQGRPWQDTWES-----56
DB 1 MNSYKNQNEYEMLDALRINNSNMCYPRYFLAKDPQMTWRTNY---KEWLNNCDSNTQF 57
QY 57 VSDIVT-----IGTYLIQFLLEPGIGPVI---FSIINKLI---90
DB 58 IGDISTYSPPEALSVRDAVLGINSVGTLSNL-----GVPLASQSGFIISRLIGIL 110
QY 91 ---PSSGQSVAALSICDLVSIIRKEVDSVLGVDGADPEGEMTAYQDYLYLHLEDWLTDK 147
DB 111 WAGPDPFFALMWL-----VEELIKSIDQVRNALRELEG-IQIMRLYQTRLOAWLVNK 165
QY 148 SNPKKLADVVKQFQAREEDFTKLAGLSRQKAEILLFTYVQAAVNHLLLRDVAKYKK 207
DB 166 NDDNRRRA-LVTQYAVDNFFEKMP-KPKERNEILLFPVYQAANLHILLRDADYFCA 223
QY 208 EWLVCPLYPGSGTDCNE---RLKAKIKETNVCVGNKGLDQIRQAGTSAEWSKIF 264
DB 224 QMWL-----GDDEIRDNYRLQGLIREYKDHCIITFYNOGLNQFNR--SNAQDWVSF 272
QY 265 NKFRREMTLAVLDIIAIPPTYDFEYKPLATSVELTREIYTDVGVY-----SGS-NYGM-- 316
DB 273 NFRFTDMTLVLDLAILPNYDPRYPLAKVELTREIYTDVGVY-----SGS-NYGM-- 332
QY 317 ERFFSFNSVEANGTRPGVLVTLQALDIYSHSINLQLGYLSQGGTGRHYEDFTKNGARQ 376
DB 333 PNNTFTAMENARRPSYTTWLNRI FVYTRTLGNMSDVNTWGGHTLVENGDSSEITH 392
QY 377 RMSGTTSNPN-RNIIFGNTDIPKISLARYAMQPFVG-----YISPRHLVSRABFFPT 429
DB 393 NFGKTDSTIPQYFNFLSVESIESLARI-----YLGGTAEANNYITSOYGVSRVIFNTSN 448
QY 430 LN-----TPLYEVNSSGYSTIESVLPGLKDL-P-SRTNYSRLSNAACVQNETSR---- 480
DB 449 INNVPGSLRYEPALPQSOTISELPG--KQPRNAGDFSHRLS---YISNFDARRSS 503
QY 481 -----VNVFGWTHSMKDNRIYDPKIQTQIPAKAFALPAGTGAG--GYVTAGPGYTG 533
DB 504 GGIIVSLTFGWAHTSMRNLRLPKITQIDAVK-----GWGNGTGFVTPGP--TGG 553
QY 534 DVVTLPYQ-ASLKIRLTSAPTNNKRYRLRYA---SGGPGPFRVERWSPSSV-----SN 583
DB 554 NLVKVSDWSHSLKVQAPQRT--SYRILRYACLVTHGDAIF-VEHSGSSHIVSFPDCSN 610
QY 584 ANFSRPA-TGGYSDFYVDT-----LVTTFNQSGVEIILQNLGSHYILVDKVEFI 632
DB 611 SS-GRPSNTLLESDFRYIDVPGIFTSPINLIRYRTQS-----FQTHAI-DKFEFI 659
QY 633 PIDIQIEKCTKQFEGDICRCEGVOSLETKEKKEIVNSLFIN 672
DB 660 FLN-----TFPN-----OSLEKREQEVDNLFIN 682

RESULT 8

AEA81457

ID AEA81457 standard; protein; 1151 AA.

XX AEA81457;
AC 25-AUG-2005 (first entry)
DT Bacillus thuringiensis Cry9 protein, cryaa2, SEQ ID NO: 13.
DE Transgenic plant; pesticide; genetically engineered microorganism; cry9;
KW endotoxin.
XX Bacillus thuringiensis.
OS US2005138685-A1.
PN 23-JUN-2005.
PD 21-DEC-2004; 2004US-00018615.
PF 22-DEC-2003; 2003US-0531807P.
PR (DUPO) DU PONT DE NEMOURS & CO E I.
XX Flannagan RD, Abad AR;
XX WPI; 2005-444221/45.
DR New isolated nucleic acid encoding a polypeptide having pesticidal
PT activity, useful for controlling pests, especially plant pests such as
PT European corn borer, diamond-back moth or fall armyworm.
XX Disclosure; SEQ ID NO 13; 114pp; English.
XX The present invention relates to the Bacillus thuringiensis Cry9-family
CC genes that encode delta-endotoxins having pesticidal activity against
CC insect pests. The invention is useful for producing pesticidal
CC compositions for controlling pests in plant such as European corn borer,
CC diamond-back moth or fall armyworm. The invention is also useful in
CC production of transgenic plant. The present sequence is the Bacillus
CC thuringiensis Cry9 protein.
XX Sequence 1151 AA;

Query Match 22.5%; Score 801.5; DB 9; Length 1151;
Best Local Similarity 31.2%; Pred. No. 8.2e-65;
Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;

QY 9 NTNEYELDGSPPNNTMSN---RYPPAKDPNIFPINLDACQGRP---WQD-TWESVSDIV 61
DB 2 NQKHGII-GASCGCASDDVAKYPLANNPYSSALNLSQNSILNWINIIGDAKEAV 60
QY 62 TGTVLIQFLLEPGIGG-IPVIPSINKLI-PSSGQSVAALSICDLVSIIRKEVDSVLS 119
DB 61 SIGTTIVSLITAPSLTGLISIVVDLIGKVLGGSSGQISDLISCDLISIDLRVSQSVLN 120
QY 120 DGVADPEGEMTAYQDYLYLHLEDWLTDKNPKLA--DVVKQFQAREEDFTKLL----- 171
DB 121 DGIADFNQSVLLYRN-YLEALDSW---NKNPNASABELTRPRIADSEFDRLTRGSLT 176
QY 172 -AGLSRQKAEITLLPTVYQAAVNHLLLRDVAKYKKEWGLVCPPLYPGSGRTDCNRLK 230
DB 177 NQGLSARQNAQIILLPSFASAAFFHLLLRDARTRYGTNWG-----LYNATFFINYQSKLV 231
QY 231 AKIKETNYVCVGNKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIFPTDYPEKY 290
DB 232 ELIELYTDYCVHYNRGFNELRQRTSATAWLEFHYRREMTLWLDIVASFSSLDITNY 291
QY 291 PLATSVELTREIYTDVGVY-----SGGNYQWERFF---SFSNVEANGTRGGLVTLWQALD 343
DB 292 PIETDFQLSRVITYTDPIGFVHRSSLRGSEWFSFVNRFANFSDL-NAIPNPRPSWFLNMI 350
QY 344 IYSHSINLQGLVLSG-----WGGTRHYEDFTKNGAF--QRMSCTTSNNPRNIIFGNTDIF 397
DB 351 ISTGSLTLPVSPSTDRARVYGSR---DRISPANSQFITEISQHTATQITLGRN--IF 406

XX	PF	15-DEC-1998;	98WO-USO26585.
XX	PR	31-DEC-1997;	97US-00002285.
XX	PA	(MYCO) MYCOGEN CORP.	
XX	PI	Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA; Muller-Cohn J;	
XX	PS	WPI; 1999-405513/34. N-PSDB; AAX83876.	
XX	PT	Method for control of European corn borer using Bacillus thuringiensis toxins.	
XX	PP	Claim 1; Page 86-90; 174pp; English.	
XX	CC	A method has been developed for the control of European corn borer (<i>Ostrinia nubilalis</i>), comprising contacting the pest with a pesticidal amount of a Bacillus thuringiensis toxin. The method is used for the control of European corn borer (<i>Ostrinia nubilalis</i>). The method can also be used for the control of other non-mammalian pests, particularly black cutworm, and other lepidopteran pests. The present sequence represents a Bacillus thuringiensis toxin from the present invention	
XX	OS	Bacillus thuringiensis serovar galleriae.	
XX	PN	US2005138685-A1.	
XX	PD	23-JUN-2005.	
XX	PP	21-DEC-2004; 2004US-00018615.	
XX	PR	22-DEC-2003; 2003US-0531807P.	
XX	PA	(DUPO) DU PONT DE NEMOURS. & CO E I.	
XX	PI	Flanagan RD, Abad AR;	
XX	DR	WPI; 2005-444221/45.	
XX	XX	New isolated nucleic acid encoding a polypeptide having pesticidal activity, useful for controlling pests, especially plant pests such as European corn borer, diamond-back moth or fall armyworm.	
XX	PS	Disclosure; SEQ ID NO 12; 114pp; English.	
XX	CC	The present invention relates to the Bacillus thuringiensis Cry9-family genes that encode delta-endotoxins having pesticidal activity against insect pests. The invention is useful for producing pesticidal compositions for controlling pests in plant such as European corn borer, diamond-back moth or fall armyworm. The invention is also useful in production of transgenic plant. The present sequence is the Bacillus thuringiensis Cry9 protein.	
XX	SQ	Sequence 1156 AA;	
XX	Query Match	22.5%; Score 801.5; DB 2; Length 1156;	
XX	Best Local Similarity	31.2%; Pred. No. 8.2e-65;	
XX	Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;		
Qy	9	NTNEYILDGSPNNMTNSN---RYPPAKDPNIPFINDACQGRP---WQD-TWESVSDIV 61	
Db	2	NONKHGII-GASNGCADDVAKYPLANNPYSSALNLNSCONSSILNWNIIGDAKEAV 60	
Qy	62	TIGTYLIQFLLEPGIGG-IPVIFSINKLI-PSSGQSVAALSICDLVSIIRKVEDSVLS 119	
Db	61	SIGTTIVSLITAPSLTGLISIVYDLICKVLGGSGQISIDLSICDLLSIIIDLRSQSVLN 120	
Qy	120	DGVADPEGETATQDYVYLHLEDMLTKSNPKLA--DVVKQFOAREEDFTKLL----- 171	
Db	121	DGIADFNQSVLLYRN-YLEALDSW---NKNPNSASAEBELTRPRIADSEFRILTRGSIT 176	
Qy	172	-AGSLRQKAIEILLPTYQAAMVHLRLLDARVKKEWGLCPPLYPGSGRTDCNERLK 230	
Db	177	NGCSLARQNAQIILLPSASAAFFHLLLRDATRYGTNG-----LYNATPINTQSKLV 231	
Qy	231	AKIKETNYTCVGNWKLQIQAGTSAEVWSKFNKRREMTLAVLDIIAIFPTDFEKY 290	
Db	232	ELIELTYDCVHWYNGFNEQLRGTSATAWLFHFHYREMTLMWLWDIVASFSSLDITNY 291	
Qy	291	PLATVELIREITDVGYY----SGNYGWERFF----SFNSVEANGTRGPGLVTWLOAID 343	
Db	292	PIETDFQLSRVIYTDPIGFVHRSSLRAGESWFSPVNRANFSDL-E-NAIPNPRESFWFLNMI 350	
Qy	344	IYSHSINLOGLYSG----WGGRPHYEDFTKGNAF--QRMSCTTSNNPNIIFGWTDF 397	
Db	351	ISTGSLTLVPSPSTDRAVWYGR--DRISPANSQFITELISGOHTATQTILGRN--IF 406	
Qy	398	KIISLARYAQMPFGVYSIPRHLSRAEFPTT---LNTFLYE--VNSSGYS----QTIES 448	
Db	407	RVDQSACLNDTTYG-----VNRAVFYHDASEGQRSVYEGYIRTGIDNPRVQNINT 459	
Qy	449	VLPGINKDLPSPSTNYSHRLSNA-----ACVQNETSRNVVFGWTHTSMKDNRIYPD 500	
Db	460	YLPGENSDI--PTPEDYTHILSTTINLTGRLQVASNRRSSLVMYGWTHKSLARNNTINPD 518	
Qy	501	KITQIPAVKAFALPAGTVAGGYTAGVGTGGVVTLPYQASLKRLTSAPTN--KNVR 558	
Db	519	RITQIIPLTKVDTRTGTGVSYVN-----DPGFIGALLQRTDHDSLGLVRLVQFPHLHQQR 573	
Qy	559	VRIRYASGGPGPRVRWRWPSSVSANFRPAT-----GGYSSFYVDVTLVTTFNQ 609	

XX	PF	15-DEC-1998;	98WO-USO26585.
XX	PR	31-DEC-1997;	97US-00002285.
XX	PA	(MYCO) MYCOGEN CORP.	
XX	PI	Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA; Muller-Cohn J;	
XX	PS	WPI; 1999-405513/34. N-PSDB; AAX83876.	
XX	PT	Method for control of European corn borer using Bacillus thuringiensis toxins.	
XX	PP	Claim 1; Page 86-90; 174pp; English.	
XX	CC	A method has been developed for the control of European corn borer (Ostrinia nubilalis), comprising contacting the pest with a pesticidal amount of a Bacillus thuringiensis toxin. The method is used for the control of European corn borer (Ostrinia nubilalis). The method can also be used for the control of other non-mammalian pests, particularly black cutworm, and other lepidopteran pests. The present sequence represents a Bacillus thuringiensis toxin from the present invention	
XX	OS	Bacillus thuringiensis serovar galleriae.	
XX	PN	US2005138685-A1.	
XX	PD	23-JUN-2005.	
XX	PF	21-DEC-2004; 2004US-00018615.	
XX	PR	22-DEC-2003; 2003US-0531807P.	
XX	PA	(DUPO) DU PONT DE NEMOURS. & CO E I.	
XX	PI	Flanagan RD, Abad AR;	
XX	DR	WPI; 2005-444221/45.	
XX	PT	New isolated nucleic acid encoding a polypeptide having pesticidal activity, useful for controlling pests, especially plant pests such as European corn borer, diamond-back moth or fall armyworm.	
XX	PS	Disclosure; SEQ ID NO 12; 114pp; English.	
XX	CC	The present invention relates to the Bacillus thuringiensis Cry9-family genes that encode delta-endotoxins having pesticidal activity against insect pests. The invention is useful for producing pesticidal compositions for controlling pests in plant such as European corn borer, diamond-back moth or fall armyworm. The invention is also useful in production of transgenic plant. The present sequence is the Bacillus thuringiensis Cry9 protein.	
XX	SEQ	Sequence 1156 AA;	
XX	Query Match	22.5%; Score 801.5; DB 2; Length 1156;	
XX	Best Local Similarity	31.2%; Pred. No. 8.2e-65;	
XX	Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;		
QY	9	NTNEYILDGSPNNMTNSN---RYPPAKDPNIPFINDACQGRP---WQD-TWESVSDIV 61	
DB	2	NONKHGII-GASNGCADDVAKYPLANNPYSSALNLNSCONSSILWINIIGDAKEAV 60	
QY	62	TIGTYLIQFLLEPGIGG-IPVIFSINKLI-PSSGQSVAALSICDLVSIIRKVEDSVLS 119	
DB	61	SIGTTIVSLITAPSLTGLISIVYDLICKVLGGSGQISIDLSICDLLSIIIDLRSQSVLN 120	
QY	120	DGVADPEGETATODYLHYLEDWLTKSNPKLA--DVVKQFOAREEDFTKLL----- 171	
DB	121	DGIADFNGSVLLYRN-YLEALDSW---NKNPNSASAEBELTRPRIADSEDFRILTRGSIT 176	
QY	172	-AGSLRQKAIEILLPTYQAAMVHLLLRDVAKYKKEWGLCPPLYPGSGRTDCNERLK 230	
DB	177	NGCSLARQNAQIILLPSFASAAFPHLLLRDATRYGTNWG-----LYNATPFINQSKLV 231	
QY	231	AKIKETNYTCVGNWKLQIQAGTSAEVWSKFNFREMTLAVLDIIAIFPTDYFEKY 290	
DB	232	ELIELTYDCVHWYNGFNELRGQTSAWLEFHRYREMTLWLWDIVASFSSLDITNY 291	
QY	291	PLATVELIREITDPVGY----SCGNYGWERFF----SFNSVEANGTRGPGLVTWLOAID 343	
DB	292	PIETDFQLSRVIYTDPIGFVHRSSLRAGESWFSPVNRAFSDLE-NAIPNPRESFWFLNMI 350	
QY	344	IYSHSINLOGLYSG---WGGRPHYEDFTKGNAF--QRMSCTTSNNPNIIFGWTDF 397	
DB	351	ISTGSLTLVPSPSTDRAVWYGR--DRISPANSQIFELISGOHTATQTILGRN--IF 406	
QY	398	KIISLARYAQMPFGVYSIPRHLSRAEFPTT---LNTFLYE--VNSSGYG---QTIES 448	
DB	407	RVDSQACNLNDITYG-----VNRAVFYHDASEGQRSVGEYIRTTGIDNPRVQNINT 459	
QY	449	VLPGINKDLPSTNTYNHRLSNA-----ACVQNETSRNVVFGWTHTSMKDNRIYPD 500	
DB	460	YLPGENSDI-PTPEDYTHILSTTINLTGLRQVASNRSSRLVMYGWTHKSLARNNTINPD 518	
QY	501	KITQIPAVKAFALPAGTVAGGVYTAGVGTGGVVTLPYQASLKRLTSAPTN--KNVR 558	
DB	519	RITQIIPUTKVDTRTGTGVSYVN-----DPGFIGALLQRTDHDSLGLRVQFPHLRQQVR 573	
QY	559	VRIRYASGGPGPRVRWRWPSSVSANFRPAT-----GGYSSFYVDVTLVTTFNQ 609	

QY 172 -AGSLSRQKAEILLPTTVQAAVHLLLRDAVKYKKGWGLVCPPLYPGSGRTDCNERLK 230
 DB 177 NGGSLARQNAQIILLPSASAAFFHLLLRDARTYGTWNG-----LYNATPPINYSKIV 231
 QY 231 AKIKEYTNYCVGWYKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIPFTYDFEKY 290
 DB 232 ELIELYTDYCVHWYKGNFELRQRTSATAWLEFHYRREMTLWLDIVASFSSLDITNY 291
 QY 291 PLATSVELTREIYTPDVG-----SGNYGWERFF---SPNSVEANGTRCPGLVTLQALD 343
 DB 292 PIETDFQLSRVIYTDPIGFVHRSSLRGESWFSFVNANFSDLE-NAIPNPRPSWFLNNMI 350
 QY 344 IYSHSINILQGLYSG-----WGTRHYEDFTKNGAF--QRMSTGTTNNPRNIIFGNTDIF 397
 DB 351 ISTGSLTLVPSPSTRARWYGSR--DRISPANSQFITEISGQHTTATQILGRN--IF 406
 QY 398 KIISLARYAMQPFVGYSPRHLVSRAPFPPTT---LNTFLYE--VNSSGYS-----QTI 448
 DB 407 RVDSQACNLNDITYG-----VNRVAFVHDASEGSRQSVYEGYIRTTGIDNPRVQNT 459
 QY 449 VLPNGKDLPPSRWYSHRLSNA-----ACVQNETSRVNVFWGHTSMKKDNRIYDP 500
 DB 460 YLPGNSDI-PTPEDYTHLSTTINLTGCLRQVANSRSLVMYGTWTHKSLARNTINPD 518
 QY 501 KITQIPAVKAFALPAGTGVAGGYVTAGCGYTGDDVVTLPYQASLKIRLTSAPTN--KNR 558
 DB 519 RITQIPLTKVDTRGTGVYN-----DPGFTGALLQRTDHSGLVLRVQFPHLRQVR 573
 QY 559 VRLYASGGPGPFRVERMSPSVSNANFSRAT-----GGYSSDFYDVLTVTFNQ 609
 DB 574 IRRVYAS---TTNIRLSVNGSFGTISQNLPMSTMLGDLRYGSPFAREFNYSIRPTASP 629
 QY 610 SGVEILIQ-NLSGYHLIVDKVEFIPIDIQIEKTKQCEGDICRCGQVSLTKKEIVNS 668
 DB 630 QDIRLTIEPSFTRQEVYVDRIEFIVN-----PTR-----EAKEDLEAAKAVAS 674
 QY 669 LF 670
 DB 675 LF 676

RESULT 12

AA82988
 ID AA82988 standard; protein; 1279 AA.

XX
 AC AA82988;

DT 12-SEP-2003 (revised)

DT 04-JUL-2000 (first entry)

XX Native Cry9Aa toxin.

XX Cry9Aa; insecticide; transgenic plants; pest control; crop protection.

XX Bacillus thuringiensis; ssp. galleria.

XX Key Location/Qualifiers

FT Misc-difference 8 /note= "Absent or unidentified amino acid"

FT Misc-difference 20 /note= "Absent or unidentified amino acid"

FT Misc-difference 35 /note= "Absent or unidentified amino acid"

FT Misc-difference 86 /note= "Absent or unidentified amino acid"

FT Misc-difference 95 /note= "Absent or unidentified amino acid"

FT Misc-difference 118 /note= "Absent or unidentified amino acid"

FT Misc-difference 118 /note= "Absent or unidentified amino acid"

XX WO200011025-A1.

XX 02-MAR-2000.

XX 24-AUG-1999; 99WO-FI000698.
 PF 24-AUG-1998; 98FI-00001809.
 PR (UNIC-) UNICROP LTD.
 XX Kuvshinov V, Kanerva A, Koivu K, Pehu B;
 PI WPI; 2000-224660/19.
 DR N-PSDB; AA293235.
 XX Modified synthetic DNA sequences comprise modification of the truncated
 PT cry9Aa gene of *Bacillus thuringiensis* for improved insect control in
 PT plants.
 XX Claim 1; Page 51-53; 90pp; English.
 XX Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
 CC gene of *Bacillus thuringiensis* ssp. galleria can be used for the
 CC production of a unique insecticidal protein having the same properties as
 CC the N-terminal domain of the insecticidal protein encoded by the native
 CC cry9Aa gene of *Bacillus thuringiensis* ssp. galleria. The insecticidal
 CC toxin works by binding to specific receptor molecules in the gut of
 CC insects with consequent formation of ion channels in the epithelium. This
 CC action leads to ion efflux and paralysis of the intestinal function,
 CC which causes death of the insect. The synthetic DNA sequences exhibit
 CC enhanced expression through improved mRNA processing, stability, and/or
 CC translation providing improved tolerance against target insects. They can
 CC be used in the production of transgenic plants capable of expressing the
 CC N-terminal domain of the insecticidal protein encoded by the native
 CC cry9Aa gene. They therefore have a role in pest control and crop
 CC protection. (Updated on 12-SEP-2003 to standardise OS field)
 XX SQ Sequence 1279 AA;

Query Match 22.5%; Score 801.5; DB 3; Length 1279;
 Best Local Similarity 31.2%; Pred. No. 9.8e-65;
 Matches 225; Conservative 137; Mismatches 253; Indels 107; Gaps 31;

QY 9 NTNEYILDGSPNNTNMSN---RYPPAKDPNIPFINDACQGRP---WOD-TWESVSDIV 61
 DB 130 NQNHGII-GASNCCGASDDVAKYPLANNPYPSALNLSQNSQILNWINIIGDAKEAV 188
 QY 62 TIGTYLIQFLPEGIGG-IPVIFSINKLI-PSSQGSVAALSICDLVSIIRKEVDSVLS 119
 DB 189 SIGTTIVSLITAPSLTGLISIVYDLIGKVLGSSGQISDLISICDLLSIIDLRVSQSVLN 248
 QY 120 DGVADPEGETAYQDYLYLHYLEDWLTDSKNPKLA--DVVKQFQAREEDFTKLL----- 171
 DB 249 DGIADFNGLVLYRN-YLEALDSW---NKNPNSASAEELRFRADSEFDRILTRGSLT 304
 QY 172 -AGSLSRQKAEILLPTTVQAAVHLLLRDAVKYKKGWGLVCPPLYPGSGRTDCNERLK 230
 DB 305 NGGSLARQNAQIILLPSASAAFFHLLLRDARTYGTWNG-----LYNATPPINYSKIV 359
 QY 231 AKIKEYTNYCVGWYKGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIPFTYDFEKY 290
 DB 360 ELIELYTDYCVHWYKGNFELRQRTSATAWLEFHYRREMTLWLDIVASFSSLDITNY 419
 QY 291 PLATSVELTREIYTPDVG-----SGNYGWERFF---SPNSVEANGTRCPGLVTLQALD 343
 DB 420 PIETDFQLSRVIYTDPIGFVHRSSLRGESWFSFVNANFSDLE-NAIPNPRPSWFLNNMI 478
 QY 344 IYSHSINILQGLYSG-----WGTRHYEDFTKNGAF--QRMSTGTTNNPRNIIFGNTDIF 397
 DB 479 ISTGSLTLVPSPSTRARWYGSR--DRISPANSQFITEISGQHTTATQILGRN--IF 534
 QY 398 KIISLARYAMQPFVGYSPRHLVSRAPFPPTT---LNTFLYE--VNSSGYS-----QTI 448
 DB 535 RVDSQACNLNDITYG-----VNRVAFVHDASEGSRQSVYEGYIRTTGIDNPRVQNT 587
 QY 449 VLPNGKDLPPSRWYSHRLSNA-----ACVQNETSRVNVFWGHTSMKKDNRIYDP 500

Db 588 YLPGNSDI-PTPEDYTHLSTTINLTGLRQVSNRRSSLVYMGWTHKSLARNNTINPD 646
Qy 501 KITOIPAVKAFALPAGTGVAGGVVGTGGDVVTLPYQASLKIRLTSAFIN--KNVR 558
Db 647 RLITQPLTKVDRGTGVSVN-----DPGFIGALLQRTDHSGLVLRVQFPHLRQQR 701
Qy 559 VRLRYASGPGPFRVERWSPSSVSNANFSRPAT-----GGYSSFDYDVLVTTFNQ 609
Db 702 IRVRVAS-----TTNIRLSVNGSFGTISQNLPSMTMLRGEDLRYGSPFAIREFNTSIRPTASP 757
Qy 610 SGVEIIQ-NLGYHLIVDKVRFIPIDIOIEKTKQCFEGDICRCEGVOSLETKEIVNS 668
Db 758 DQIRLTIEPSIRQEVYVDRIEFIPVN-----PTR-----EAKEDLEAAKAVAS 802
Qy 669 LF 670
Db 803 LF 804

RESULT 13

AAV83039

ID AAV83039 standard; protein; 652 AA.

XX AC

AAV83039;

DT 04-JUL-2000 (first entry)

XX Cry9Aa toxin N-terminal fragment.

DE Cry9Aa; insecticide; transgenic plants; pest control; crop protection.

KW Synthetic.

OS Bacillus thuringiensis; ssp. galleria.

XX Key

FH Location/Qualifiers

FT Misc-difference 650

FT /note= "Position is either encoded by a stop codon or
absent or unidentified amino acids"

XX WO200011025-A1.

XX 02-MAR-2000.

XX 24-AUG-1999; 99WO-FI000698.

XX 24-AUG-1998; 98FI-00001809.

XX (UNIC-) UNICROP LTD.

XX Kuvshinov V, Kanerva A, Koivu K, Pehu E;

XX WPI; 2000-224660/19.

XX N-PSDB; AA293234.

PT Modified synthetic DNA sequences comprise modification of the truncated
PT cry9Aa gene of *Bacillus thuringiensis* for improved insect control in
PT plants.

XX Disclosure; Fig 4; 90pp; English.

XX Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
CC gene of *Bacillus thuringiensis* ssp. galleria can be used for the
CC production of a unique insecticidal protein having the same properties as
CC the N-terminal domain of the insecticidal protein encoded by the native
CC cry9Aa gene of *Bacillus thuringiensis* ssp. galleria. The insecticidal
CC toxin works by binding to specific receptor molecules in the gut of
CC insects with consequent formation of ion channels in the epithelium. This
CC action leads to ion efflux and paralysis of the intestinal function,
CC which causes death of the insect. The synthetic DNA sequences exhibit
CC enhanced expression through improved mRNA processing, stability, and/or
CC translation providing improved tolerance against target insects. They can
CC be used in the production of transgenic plants capable of expressing the

CC N-terminal domain of the insecticidal protein encoded by the native
CC cry9Aa gene. They therefore have a role in pest control and crop
CC protection
XX Sequence 652 AA;

Query Match 22.2%; Score 789.5; DB 3; Length 652;

Best Local Similarity 31.6%; Pred. No. 4.2e-64;

Matches 214; Conservative 130; Mismatches 243; Indels 91; Gaps 28;

Qy 18 GSPNNTNMGN--RYFPKADPNIPPINLDACQRRP---WQD-TWESVDIVTIGTYLQF 70

Db 2 GMPNCCASDDVAKYPLANNPYSSALNLSQNSILNWINIIGDAAKEAVSIGTIVSL 61

Qy 71 LLEPGIGG-IPVIFSIINKLI-PSSQSVAAALSTCDLAVSIIRKEVDSEVSLSDGVADPEGE 128

Db 62 ITAPSLTGLISIVYDLIGKVLGGSGQISDLSICDLLSIIDRVSVSLNDGADFNGS 121

Qy 129 MTAYQDYLYHLEDMLTDSKNPKKLA--DVVKQFOAREEDFTKLL-----AGSLSRQK 179

Db 122 VLLYRN-YLEALDSW---NKNPNSASAEELRTFRITADSEFDRLITRGSNTGSLARQN 177

Qy 180 AEILLPTYVQAAVHLLLRDAVKYKXGVLVCPPLYPGSGRTDCNERLKAKIKEYTNY 239

Db 178 AQILLPSFASAAFFHLLLRDARTYGTNWG-----LYNATPFYNYQSKVELIELYDY 232

Qy 240 CVGWNKGLDQIRQAGTSABVWSKFNKFRREMTLAVLDIIAIPPTYDFEYKPLATSVLT 299

Db 233 CVHWYNRGFNELRQRTSATWLEFHYRREMTLVLDIVASFSSLDITNYPITDFQLS 292

Qy 300 RIYTDPCVY---SGNGYWERFF---SFNSVEANGTRCGPLVTVLQADIDYSHSINLQ 352

Db 293 RVITYDPIGVHRSSLRGSEWFSFVNANFSDLE-NAIPNRPFSWFLNNMIISTGSLTLP 351

Qy 353 LGYLSG---WGTRHYEDFTKNGAF--QRMSEGTTSNNPRNIFGNTDIFKIISLARYA 406

Db 352 VSPSTDARVWYGSR--DRISPANSQFITEILISQHTTATQTLGRN--IFRVDQACNL 407

Qy 407 MQPFVGYSPRHLVSRAEFFPTT---LNTFLYE--VNSSGYS---QTISVLPQINKDL 457

Db 408 NDTTYG-----VNRAVFHDASEGSRVSEGYIRTTGIDNPRVQNTIYLPGENSDI 460

Qy 458 PPSRTNYSRLSNA-----ACVQNETSRVNVFVGTHTSMKKDNRIYDPKTIQIPAVK 509

Db 461 -PTPEDYTHLSTTINLTGLRQVSNRRSSLVYMGWTHKSLARNNTINPDRIQIPUTK 519

Qy 510 APALPAGTGYAGGYVTAGPGYTGDDVVTLPYQASLKIRLTSAFTN--KNYRVLRYASGG 567

Db 520 VDRGTGVSVN-----DFGFIGALLQRTDHSGLVLRVQFPHLRQYRIRVRYAS-- 572

Qy 568 PGFPRVERWSPSSVSNANFSRPAT-----GGYSSFDYDVLVTTFNQSGVEIIQ- 617

Db 573 --TTNIRLSVNGSFGTISQNLPSMTMLRGEDLRYGSPFAIREFNTSIRPTASPDQIRLTIEP 630

Qy 618 NLSGYHLIVDKVEFIPID 635

Db 631 SFIRQEVYVDRIEFIPVN 648

RESULT 14

AAV83040

ID AAV83040 standard; protein; 656 AA.

XX AC

AAV83040;

XX 04-JUL-2000 (first entry)

XX Synthesised Cry9Aa toxin.

DE Cry9Aa; insecticide; transgenic plants; pest control; crop protection.

XX Synthetic.

XX *Bacillus thuringiensis*; ssp. galleria.

PT for producing organisms with pesticide resistance.

XX
PS Claim 12; SEQ ID NO 22; 178pp; English.

This sequence represents an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

AA
SQ Sequence 671 AA;

Query Match 22.0%; Score 782.5; DB 8; Length 671;

Best Local Similarity 33.1%; Pred. No. 2e-63;

Matches 248; Conservative 111; Mismatches 221; Indels 169; Gaps 40;

QY 15 ILDGSPNNNTMSN---RYPFAKDPNIFPINLDACQGRPWQDTWES---VSDIVT----- 62

Dd
Db

1 MLDALRINSMNSCYPRYPLAKDPQMTMRNTNY----KEWLNMCDNTOFGDISITYSSPE 57

Oy 63 -----IGTVLIQFLLEPGGIPVI---FSINKULI-----PSSQSVA 98
 :||| |||::|||
 ::||| |||:

D**b** 58 AALSVRDAVLTGINSVGITLSNL-----GVPLASQSGFIISRLTIGILWAGDPPEALM 110

Qy 99 ALSICDLVSIIRKEVDESVLSDGVADFEGETAYQDYIHLHYLEDWLTDKSNPKKLADWVK 158

DB 111 VL---VVELIKSIDQVRENALRELEG-LOGIMRLYQTRLQAWLVNKDDNRRA-LVT 164

[illegible]

00	00	105	QIAI VDNFF ENWME - NF NERNFF EILULLPVI AQAAVNHLLI LERDADY FGAQWQL-----	219
00	219	GSRTDCNE - --RI KAKTKEVTNYCVGWYKNCI NOI BOACTSA EYWSKYNKEEDDEMTT AV	075	

217	--GDEIRDNYIRJLOGLFREYKHCITFYNOGLNOFR--	SNADQWSENFRTDMLTY	272
218	QGNKDCNE--AAWAKKKEITIRICVQWINGNSQIKQGISAEVWNSNFWKREMLLAV	Z71	

276 LDLIAIPTYDFEKYPLATSVELTREIYTDPVGY-----SGG-NYGM--ERFFSFNSVEA 327 QY

```
Db      273 LDAILFNYPDRRYPLAVKTELREVVYDTPVGFTVLESGGRYPWYNPNNTTAMEN 332
```

QY 328 NGRGPGIWTWLQAIIDIIYSHSINLQLGLSGWGCTRHYEDFTKNGCAFQFMGSGTTSNP- 386

D_b 333 NARRRPSYTTWLNRFVYRTTLGNMSDVNRNIGWGHTLVENGNDGSEITHNFGKDSITPI 392

QY 387 RNIIFGNTDIFKIIISLARYAMQFVG-----YSIPRHVLSRAEFTPTLN-----TFLYE 436

Db 393 QYFNFANLVSFIESLARI---YLGGEANNYITSQGVSRVIENTSINNVPGLRYE 448

Qy 437 VNSSGYSTIESVLPINKDLP-PSRTNYSHRLSNAACVQNETGR-----VNVPFGW 486

Db 449 VPANLPSQTILSELPG--KDKPRNAGDFSHRLS---YISNFDARRSSGGGIVSLLTFGW 503

487 THTSMKDNRIYDKITOI PAVKAFALPAGTGYAG--GYVTAGPGYTGDDVITLPYQ-AS 543

DB	504	AHTSMDRRNRLEPKITQIDAVK-----GCGNIGFVPGP--TGGNLVKYSDSWHS	553
Qv	544	IKWIDI TGA DTNKNVYVBI DVA ---SCCCDCEBVEVDGDCGCV	593
		CHANGERRDA	600

[illegible]

Qy	594	YSSFDYVDV"------LVTNENOSGVEIIHONLSGYHLIVDKVFETPIDIOIEKCTK	643
DD	JJ4	ZNAVAFQAQI---SIAIRAKRIACAVIHNDALF-VENSGSSHHVSFFDCSSNS-GRFSNIILL	807

```

610 ESDFRYIDVPGIFTPSINPLIRVTQS-----FGTHAI-DKFEF.IPLN----- 651
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```

QY 644 CQFEGDICRCEGVQSLETKKEIVNSLFIN 672

Db 652 -TFPN-----QSLEKREQEVNDLFIN 671

Search completed: December 15, 2005, 10:14:38
Job time : 201 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2005, 09:49:20 ; Search time 235 Seconds
(without alignments)
2017.511 Million cell updates/sec

Title: US-10-782-141-3
Perfect score: 3556
Sequence: 1 MKNMNSYQNTNEYILDGSP.....CEGVOSLETKEIVNSLFIN 672

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1872	52.6	666	2 Q8VM62_BACTA	Q8VM62 bacillus th
2	1610.5	45.3	666	2 Q7X3F7_BACTA	Q7X3F7 bacillus th
3	940.5	26.4	686	2 Q75Q05_BACTE	Q75Q05 bacillus th
4	918.5	25.8	674	1 C24AA_BACTJ	Q87905 bacillus th
5	801.5	22.5	1156	1 CR9AA_BACTG	Q99031 bacillus th
6	789.5	22.2	675	2 Q6BCH5_BACTU	Q6bch5 bacillus th
7	773	21.7	1157	1 CR8AA_BACUK	Q45704 bacillus th
8	772.5	21.7	1239	1 CR1BB_BACTU	Q45739 bacillus th
9	772.5	21.7	1233	1 CR1BC_BACTM	Q45774 bacillus th
10	756.5	21.3	719	1 CR1ID_BACTU	Q9xd11 bacillus th
11	756	21.3	1228	1 CR1BA_BACTK	P0a373 bacillus th
12	755	21.2	1228	2 Q93NM5_BACTU	Q93nm5 bacillus th
13	754	21.2	1144	2 Q8KZL7_BACTG	Q8kz17 bacillus th
14	754	21.2	1228	1 CR1BA_BACTE	P0a374 bacillus th
15	754	21.2	1228	2 Q93T75_BACTE	Q93t75 bacillus th
16	752.5	21.2	1160	1 CR8CA_BACTP	Q45706 bacillus th
17	752.5	21.2	1160	2 Q6R2R6_BACTU	Q6r2r6 bacillus th
18	745.5	21.0	1231	2 Q8KNY2_BACTU	Q8kny2 bacillus th
19	743.5	20.9	1231	1 CR1BD_BACTZ	Q9z3z5 bacillus th
20	731	20.6	675	1 C28AA_BACTJ	Q87906 bacillus th
21	729	20.5	1169	1 CR8BA_BACUK	Q45705 bacillus th
22	723.5	20.3	849	2 Q6PYW8_BACTK	Q6pyw8 bacillus th
23	723.5	20.3	1227	1 CR1BE_BACTU	Q85805 bacillus th
24	716	20.1	719	1 CR1IA_BACTK	Q45752 bacillus th
25	716	20.1	719	2 Q6X181_BACTU	Q6x181 bacillus th
26	716	20.1	719	2 Q546K2_BACTK	Q546k2 bacillus th
27	716	20.1	746	2 Q4W4S8_BACTU	Q4w4s8 bacillus th
28	715	20.1	719	2 Q85796_BACTK	Q85796 bacillus th
29	715	20.1	719	2 Q5S1W9_BACTU	Q5s1w9 bacillus th
30	714	20.1	720	2 Q4LDH4_BACTU	Q4ldh4 bacillus th
31	713	20.1	719	2 Q93NJ5_BACTU	Q93nj5 bacillus th

32	710.5	20.0	719	1 CR1IB_BACTE	Q45709 bacillus th
33	707.5	19.9	1138	1 CR7AB_BACUK	Q45708 bacillus th
34	707	19.9	719	2 Q9F0P8_BACTU	Q9f0p8 bacillus th
35	704.5	19.8	660	2 Q8ROU6_BACTA	Q8rou6 bacillus th
36	698.5	19.6	719	2 Q8KY61_BACTU	Q8ky61 bacillus th
37	692	19.5	1163	1 C26AA_BACTF	Q9X597 bacillus th
38	689.5	19.4	1138	1 CR7AB_BACUA	Q45707 bacillus th
39	682.5	19.2	1138	1 CR7AA_BACTU	Q03749 bacillus th
40	680	19.1	652	1 CR3BB_BACTU	Q06117 bacillus th
41	676	19.0	1215	1 CR1KA_BACTM	Q45715 bacillus th
42	675.5	19.0	1340	2 Q589X2_PAEPP	Q589x2 paenibacill
43	674	19.0	1163	2 Q5XLA8_BACTP	Q5xla8 bacillus th
44	673	18.9	648	1 C19AA_BACTJ	Q03207 bacillus th
45	664.5	18.7	659	1 CR3BA_BACTO	P17969 bacillus th

ALIGNMENTS

RESULT 1
Q8VM62_BACTA
ID Q8VM62_BACTA PRELIMINARY; PRT; 666 AA.
AC Q8VM62;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Putative mosquitoicidal toxin (Fragment).
GN Names-cry40A;
OS Bacillus thuringiensis (subsp. aizawai).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1433;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ito T., Sahara K., Asano S., Bando H.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AB074414; BAB72018.1; -; Genomic_DNA.
DR HSSP; Q06117; 1J16.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR000834; Peptidase_M14.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 666 AA; 75311 MW; A87853FAE8FA4A1D CRC64;

Query Match	52.6%;	Score 1872;	DB 2;	Length 666;
Best Local Similarity	57.0%;	Pred. No. 2.4e-127;		
Matches	392;	Conservative	91;	Mismatches 161; Indels 44; Gaps 15;
QY	5	NSYQNTNEYILDGSPNNTMNSRYPFAKDNPINLDACQGRPMQDTWESVSDIVTIG	64	
DB	1	NSYENKNEYELSSNNTMNPYPFANDRDMSTWMSFNDCCQGISWDEWESAETISIG	60	
QY	65	TYLIQFLLEPGIGIPVIFSIINKLIPSSCQSVAAISICDLVSIIRKEVDSVSDGVAD	124	
DB	61	IDLIEFLMEPLSGGINTLFIIGKLIPTNHQSVSALISICLLSIIRKEVADSVLSAICR	120	
QY	125	F-EGEMTAYQDYVLYHLEWLT-----KSNPKLADVVKQFOAREDEFTKLLAGSLSRQ	178	
DB	121	FUDGKLKNRYEYLYPYLEAWLKDGPQLQKNTNSDIGOLVKYFELSEDFNEILGGLARN	180	
QY	179	KAEILLPTVQAAVHLLLRDAVKYKKEW-----GLVCPPLYPGSG---RTDCNER	228	
DB	181	NAQILLPLFCASCKQLLLLRDAVQEYEQWFPFLSAENVRSSELISNSGCDFTGDIYER	240	

QY 229 LKAKIKEYTNYCVGNKGLDQI ROAGTSAEWSKFNKFRREMTLAVLDIIAIPPTDYDE 288
 DB 241 LKCKIAEYTDYCEYQAGLNOIKOAGTGADTWAKFNKFRREMTLTVLDIIAIFQTYDFK 300
 QY 289 KYPLATSVELTREIYTDVPVYSGNGWERFF--SFNSVEANGTRGPGVLTWLOAIDIYS 346
 DB 301 KYPLPHTVELTREIYTDVPVYSSGYTSMUKYWTGAFNTLEANGTRGPGVLTWLRISGIYN 360
 QY 347 HSINLQLGSLGSGWGTTHYEDFTKNGAFORMSGTTSNNPRNI IFGNTDIFKIIISLARYA 406
 DB 361 EYVS--RYFSCWGTGTHYEDFTKNGAFORMSGTTSNDLRI SPNSDIFKIES---KA 414
 QY 407 MOPFVG--YSIPRHLVSRAPFPTTLNTFLYEVNSSGY-SOTIESVPGINKDLPPSRTN 463
 DB 415 IMNLVGEINARPEYVSRAEFSESTAFIYLDAGNSGLSSMTITSKLPKI-KNPEFSYRD 473
 QY 464 YSHRLSNAACVQNETSRVNVFGWTHTSMKKNRIYDPDKITQIPAKAFALPAGTGVAGGY 523
 DB 474 YSHRLSNAACVAGNSRINVIWTHTSMSKYNLIYDPDKITQIPAKAFDI-SDTG--PGQ 530
 QY 524 VTAGPGYTGDDVVTLPYQASLKIRLTSAPTNNKYNRLRYASGPGPFRVERWSPSSVSN 583
 DB 531 VIAGFGHTGNNVSLPYYSRLKIRLIPASTNNKYNLVRVYTSNGLLVERWSPSSIIN 590
 QY 584 ANFSPATGYSYSSFDYDVTLTFTFNQSGVEIIQNLSGVLHVDKVEFIPIDIEKCTK 643
 DB 591 SYFFLPSTGPGDSFGYDVTLTFTFNQSGVEIIQNLD-TPINVDKVERIPVN----STA 644
 QY 644 COFEGDICRCGCVQSLEYKKEIVNSLFI 671
 DB 645 LEYEGK-----QSLKRAQDVNDLFV 665

RESULT 2

QYX3F7 BACTA
 ID Q7X3F7_BACTA PRELIMINARY; PRT; 666 AA.
 AC Q7X3F7;
 DT 01-OCT-2003 (TremBLrel. 25, Created)
 DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
 DE Putative mosquitoicidal toxin.
 GN Name=cry40-like;
 OS Bacillus thuringiensis (subsp. aizawai).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=1433;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Bun1-14;
 RA Ito T., Sahara K., Amano S., Bando H.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB112346; BAC77648.1; -; Genomic DNA.
 DR GO; GO:0006787; F:hydrolase activity; IEA.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR GO; GO:0030435; P:sporulation; IEA.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin.C.
 DR InterPro; IPR005639; endotoxin.N.
 DR Pfam; PF03944; Endotoxin C; 1.
 DR Pfam; PF00555; Endotoxin M; 1.
 DR Pfam; PF03945; Endotoxin N; 1.
 SQ SEQUENCE 666 AA; 75432 MW; F6E9E33309D06CDF CRC64;

Query Match 45.3%; Score 1610.5; DB 2; Length 666;
 Best Local Similarity 50.6%; Pred. No. 2.6e-108;
 Matches 356; Conservative 82; Mismatches 194; Indels 71; Gaps 20;

QY 4 MNSYQNTWEYELDGSNNNTNSNRYPPFAKDNIPINLDACQRPWQWTWESVDIVTI 63
 DB 1 MNSYQNKWEYELKSSPNNNTNIPNRYPPFANDRDMSPMNDCCGSPWNDWESTASFTGI 60

QY 64 GYLLIQFLPEIGGIPVIFSIINKLIPSSGQSVAAALSCDLVSIIRKEVDESVLSDGVA 123
 DB 61 GIDLITFLGPEISITGNLIFSIVIGKLLP-SGNVVASLSICDLLSIIRKEVDESVLSDAYG 119
 QY 124 DPEGEMTAYQDYVLYHYLEDMLTDKSNP---KKLADVVKQFOAREEDFTKLKAGSLRQKA 180
 DB 120 DFGVNNVQTYLLTSLKKWL-DAGKPTTGQLLTDVTKHFEFSEREFNALLKSLSRPKG 178
 QY 181 EILLPTTYQAAANVHLLLRDVAVKKEW-----GLVCPPLYPGSGRTDCNERL 229
 DB 179 EILLPTTYQGANLHLLLRDVFQYKAWKEKELRTENVESELISPSF-----DYEGR 231
 QY 230 KAKIKEYTNYCVGNKGLDQI ROAGTSAEWSKFNKFRREMTLAVLDIIAIPPTDYDEK 289
 DB 232 KEQLAEHINHCITWTYQAGLNQIKESGTSSTENLKNKFRREMTLSVLDDIIAIPPTDYDFEN 291
 QY 290 YPLATSVELTREIYTDVPVYSGNGWERFFS--FNSVEANGTRGPGVLTWLOAIDIYSH 347
 DB 292 YKSETHIELSREVYTDVPVYN---GWEQNLNGENTLEANGTRGPGVLTWKKIDIFTD 347
 QY 348 SINLQLGY-----LSGWGGTRHYEDFTKNGAFORMSGTTSNNPRNI IFGNTDIFKIIISL 402
 DB 348 EYTESGSPVAILRGWAGTRHYEYTGSSNTLQIRISGTTSDVSNIDFINSRIFITSL 407
 QY 403 ARYAM-----OPFVGYISIPRHLVSRAPFPTTLNTFLYEVNSSGY-SOTIESVLPKINK 455
 DB 408 ARYALAGAAAGNP---GSPRYRVSRVFRSTGRYTFLYEVNPSGISSMTIESKLPQVK 463
 QY 456 DLPPSRNTYSHRLSNAACVQNETSRVNVFGWTHTSMKKNRIYDPDKITQIPAKAFALPA 515
 DB 464 --ATGFTDYFNRLSNAACVQFCTSRVNVYGMWTHISMGEYVYVPNKITQIPAKAWEI-R 520
 QY 516 GTGAGGYVTAGPGYTGDDVVTLPYQASLKIRLTSAPTNNKYNRLRYASGPGPFRVER 575
 DB 521 GT-----SSVAGPGHTGNNLKVMSHVSWSIIFTKQOL-KRVRVRIYASDGNQCLAMRR 575
 QY 576 W--SPSSVSNANFS--RPATGG--YSSFDYDVTLTFTFNQSGVEIIQNLSGVLHVDKV 629
 DB 576 WRGGPGYQEARHTVQRTFSGSMYDYSFKYLDIFTWPAEDYDFTDLTDLGSGGALYDKI 635
 QY 630 EPIPIDIQEKCTKQFEGDICRCGCVQSLEYKKEIVNSLFIN 672
 DB 636 EPIPDDL-----TTLEYEE-----RNLEKTKNAVNDLFTN 666

RESULT 3

QY5Q05_BACTE
 ID Q75Q05_BACTE PRELIMINARY; PRT; 686 AA.
 AC Q75Q05;
 DT 05-JUL-2004 (TremBLrel. 27, Created)
 DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
 DE Putative mosquitoicidal toxin.
 GN Name=cry4Ba like;
 OS Bacillus thuringiensis (subsp. entomocidus).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=1436;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=INA288;
 RA Ikeya T., Yamaya K., Ito T., Sahara K., Bando H., Amano S.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=INA288;
 RA Tomonori I., Kumiko Y., Takeshi I., Ken S., Shin-ichiro A.,
 RA Hisanori B.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB161456; BAD08532.1; -; Genomic DNA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0005102; F:receptor binding; IEA.

DR GO:0006952; P:defense response; IEA.
 DR GO:0009405; P:sporulation; IEA.
 DR GO:0030435; P:sporulation; IEA.
 DR InterPro: IPR001178; Endotoxin.
 DR InterPro: IPR005638; Endotoxin_C.
 DR InterPro: IPR005639; Endotoxin_N.
 DR Pfam: PF03944; Endotoxin_C; 1.
 DR Pfam: PF00555; Endotoxin_M; 1.
 DR Pfam: PF03945; Endotoxin_N; 1.
 SQ SEQUENCE 686 AA; 78023 MW; 1F0FD65618AEAD2 CRC64;

Query Match 26.4%; Score 940.5; DB 2; Length 686;
 Best Local Similarity 34.3%; Pred. No. 1.7e-59;
 Matches 252; Conservative 101; Mismatches 230; Indels 151; Gaps 26;

QY 4 MNSYQNTNEYELDGSPPNNTNMSNRYPPFAKDNIIPPIN-----LDACQ-----GRPWQD 52
 DB 1 MNSYQNKNEYEILENAPSNTNPNRYPPFANDPNAMKNGYKDWLDICNPEYRYSNP--E 58
 QY 53 TWESVSDIVTIGTYLQFLLEPGIGIPV-----IFSINKLIPSS-----G 94
 DB 59 AYRNTKAAMFCVGLVSTIL--GVLGGPISVTLGALIGVTVAVLEFIPADEYDNTKETWG 116
 QY 95 QSVAAISICDLVSIIRKEVDESVLSGVADFGEMTAYQDYLYLHLEDLWLDTKSNPKLA 154
 DB 117 VLIAAIK-----ELIVEEIKGEAMNAKALDGLYKVMKNYD-NKLNVMKNGDKSPVEQN 170
 QY 155 DVVKGFQAREEDFTKLAGLSRQAEILLTPTTYQAAVHLLLRDAVYKKEGLVCP 214
 DB 171 EIQRVFAEDTNSFL--LLISQFOQLGHEVSFLFVAFVAAHLLLRDVSIGKGYT-N 228
 QY 215 PLYPG--SGRTDNERLAKIENYNYCVGWKNGLDQIRQAGTSAEV--WSKFNFRREM 271
 DB 229 NIEGYHSDQDWTQ-----DYTYAVDTNKGLEEAANKIKNQKLDWDFNQYRRDM 281
 QY 272 TLAVLDIIAIFTYDFEKYPLATSVELTREIYTDVGY-----SGNGYMERFES 321
 DB 282 TLTVLDVIALFTYDVRKYPISTKVELTREIYTDMINYNPNFMTNVEGQRFAGYVAQ 341
 QY 322 FNSVEANGTRGPGVLTWLAQDIYSHSINLQGLYSGWGTRH---YEDFT-KGNGAFOR 377
 DB 342 FNSIENALTREPHLFTLKEVTGYFYAQYQQQSFMTGIGNTSYRTNYEDYPPSGPLHGV 401
 QY 378 MSGTTSNNPRNIIFGNTDIFKILSLARYAMQFVGYSGYSPRHLVSRAPPTTLNTELYEV 437
 DB 402 YAGDTA---RSVDNNGKDVYSYS-----TWPPLETNNHVEL 436
 QY 438 -----NSS-----GYSOTIESVLPINKD--- 456
 DB 437 RPTAYYFGVKGRHDATDRRTGNSQKILGEDSKTGRTATGPSYFI-SEIYYDKETNE 495
 QY 457 -LPPSRNTYSHRLSNAACVQNETSRVN-----VFGWTHTSMKKNRIYDPDKIT 503
 DB 496 TIRTPKYNHRLSYISAYATDCGRISGVRGDCFRTPQMCATWTHVSADPYNTIHPDKIT 555
 QY 504 QIPAKAFALPAGTYAGGYVTAGGYTGGDVVTLTPYQASLKIRLTSAPTNKYRVLAY 563
 DB 556 QISAVKAFYI-WDQT--EGQVVGSGPFTGGDLVKLFPYNARLKIRLKPSTSTSKYRVRY 612
 QY 564 ASGGPGPRVERWSSVSNANFSRPATGG---YSSFDVDTLVTENOSGVEIIIONLS 620
 DB 613 ASMGAGTURAEMKSPYGSVFSNFAYEYTGDSNKNFNKYLETSLSSFNISGVVEIIIONLS 672
 QY 621 GYHLIVDKVERFIPI 634
 DB 673 SSQILVDKLEFIPI 686

RESULT 4
 C24AA BACTJ
 ID C24AA BACTJ STANDARD; PRT; 674 AA.
 AC O87905;
 DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Pesticidal crystal protein cry24Aa (Insecticidal delta-endotoxin
 DE CryXIVA(a)) (Crystalline entomocidal protoxin) (Crystal protein)
 DE (Insecticidal protein Jcg72) (Fragment).
 GN Name=cry24Aa; Synonyms=cryXXIVA(a);
 OS Bacillus thuringiensis subsp. jegathesan.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=56955;
 RN [1]
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Kawalek M.D., Gill S.S.;
 RP "Isolation and characterization of insecticidal genes from Bacillus
 RT thuringiensis subsp. jegathesan.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
 CC epithelial cells of insects.
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
 CC sporulation and is accumulated both as an inclusion and as part of
 CC the spore coat.
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
 CC terminus.
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.
 CC -----
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: U88188; AAC61891.1; -; Genomic_DNA.
 DR HSP: Q06117; LJI6.
 DR InterPro: IPR001178; Endotoxin.
 DR InterPro: IPR005638; Endotoxin_C.
 DR InterPro: IPR005639; Endotoxin_N.
 DR Pfam: PF03944; Endotoxin_C; 1.
 DR Pfam: PF00555; Endotoxin_M; 1.
 DR Pfam: PF03945; Endotoxin_N; 1.
 DR Sporulation; Toxin.
 KW NON_TER 674 674
 FT SQ SEQUENCE 674 AA; 75959 MW; DA3904DAB891C978 CRC64;

Query Match 25.8%; Score 918.5; DB 1; Length 674;
 Best Local Similarity 33.2%; Pred. No. 6.6e-58;
 Matches 239; Conservative 115; Mismatches 270; Indels 95; Gaps 20;

QY 4 MNSYQNTNEYELDGSPPNNTNMSNRYPPFAKDNIIPPIN-----LDACQGRPWQDTWESV 57
 DB 1 MNSYQNKNEYEILESSQNMMNPNRYPPADDPNVMKNGYKDWVNECEG-----SNISP 55
 QY 58 SDIVTIGTYLQFLLEPGIGIPVIFSINKLIPSSG-----QSVAAISICDLVSIIR 110
 DB 56 SPAAALTSKIVSIVLTKLAKA--VASSLADSIKSSLSGISTITENNVSQVMVQVHQIIN 113
 QY 111 KEVDESVLSDGVADFEGETAYQDYLYLHLEDLWLDTKSNPKLADVVKQFQAREEDFTKL 170
 DB 114 RRIQETILDLGSSSLNGLVAIYNRDYLGALEANNKNSINITYQTNVAEAFKTYEREFFTK 173
 QY 171 LAGLSRQKAEILLPTTYVQAAVHLLLRDAVYKKEGLVCPPLYPGSGRDTDCNERLK 230
 DB 174 LKGIYRTSSQITLPTTQAAVHLLSMURDAVMYQEGWNL-----QSHINYSKELD 225
 QY 231 AKIKEYTNYCVGWKNGLDQIRQAGTSAEVSWKFNKFRREMTLAVLDIIAIFTYDFEKY 290
 DB 226 DALEDYTNVCVEYTKGLNALR--GSTAIDWLEFNSFRDMLVLDLVAIFPNYPVRY 283
 QY 291 PLATSVELTREIYTDVPGYSGG-NYG-W-----ERFESFNVSVEANGTRGPGVLTWLAQDI 344
 DB 284 PLSTKISLSRKIYTDVGRDTSFSGDWTNTGTLANFNDLREVEVTDSPSLVKWLGDMTI 343
 QY 345 YSHSINLQGLYSG-----WGTTHYEDFTKNGAFQRMSTGTSNPNRIIFGN---TD 395


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RESULT 6
Q6BCH5 BACTU PRELIMINARY; PRT; 675 AA.
ID Q6BCH5
AC Q6BCH5
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Delta-endotoxin.
GN Name=cry24-like;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=96-OK-85-24;
RA Ohgushi A., Saitoh H., Wasano N., Ohba M.;
RT "Cloning and characterization of novel cry genes from a mosquitocidal
RT Bacillus thuringiensis serovar sotto strain."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB185105; BAD32657.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 675 AA; 75906 MW; E983D92F9053AEE8 CRC64;

Query Match 22.2%; Score 789.5; DB 2; Length 675;
Best Local Similarity 32.1%; Pred. No. 1.6e-48;
Matches 235; Conservative 106; Mismatches 270; Indels 121; Gaps 27;

QY 4 MNSYQNTWEYELDQSPNNTNSNRYPPAKDNPFPIN-----LDACOG-----RPQD 52
DB 2 VNPYQKSESVFYEHSHNQKQIPNRYPTNPNNAVMKNGYKDWNECEGSNVSPSAA 61
QY 53 TWESVSDIV--TIGYLIQFLLEPGIGGIPVIFSIINKLIPSSGOSVAALSICDLVSIIR 110
DB 62 VTSALISIVLTKALVSSLVD-AIKSSLGISEVITK-----NNVSQSMELVNLIN 114
QY 111 KEVDESVLSDGVADPEGEMTAYQDYLYHLELDLTKSNPKKLADVVKQFQAREEDFTKL 170
DB 115 RRIQETINDLSASLGLMSYK-RYLNALAEWDKSNITLQENVIEEFKVESRFFEN 173
QY 171 LAGLSRQKAEILLPTVQVQANVHLLLRDVKYKKGWGLVCPPLYPGSGRTDCNERLK 230
DB 174 LKGIYRTSSSQITLLPTFAQANLHLSMLRDVAVMYQEGWNL-----QSHLDYKMWLD 225
QY 231 AKIKETNYCVGWYKGLDQIRQAGTSAEWSKFNKPREMTLAVLDIIAIPPTDFPKY 290
DB 226 IALDKYNTYCEVYNRGNLALR--GSTALDMLFNSFRDMTLVLDLVAIFPNYDPVQY 283
QY 291 PLATSVELTREIYTPDVGYSG---GNVGV---ERFFSFNSVEANGTRGCLVTLWLOAI 342
DB 284 PLPTKIGLSRKIYTPDVTTRDTPGN--WLTDLTLANFDLDRDVTDSPLSVKWLVD 341
QY 343 DIYSHSINLQIGY-LSGNGGTR-----HYEDF--TKNGAFAQRMGTSTNNPRNIIFGN 393
DB 342 NIYGAID---SYPISGPGERIGVWYGNMNSFVLTSGRSLSYMYGEIAHEDPITNIRD 398
QY 394 TDIFKI-----ISLARYAMPQFVGYISPRHLVSRABFPPTLTNTFLVNSNGVSQIE 447
DB 399 NDIYKVDLRAAYATIRNALDSTFG-----VSSSHFFNVGNKGLYQSKQYPSYPT 451
QY 448 SVLPGINKDLPPSRNTYSHRLSNAACVQNETSRNVFG-----WHTSMKKDNRIYP 499
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452 ITFPG-BESLEGVNDYSHLLCNVQNTTGLRLQTSARGRSLSHAWTHKSLNPKNIIAA 510
500 DKITQIPAVKAFALPAGTGVAGVVTAGPGVGTGDDVTLTPYQASIKRLTSAPTNKN--- 556
511 DKITHIPAVKGSNLSASSA-----VIKPGFTGDLRLGPNQFVDYILT--PDNPQVSQ 563
557 --YRVLRLYASGGPGPRVERW-----SPSSVSNANFSRPATGGYSSFDYVD 602
564 IYFDVRLRYACMGGANILIQFMKNKWEIGVLVSTTSLENLK-----YENFAYITT 615
603 -LVTTFNQSQVEIILION-LSGYHLIVDKVRFIPIDIOIEKCTKQCFEGDICEBVGQSLE 660
616 RLSFTFGQGGYNMSIYNPTSNPNVIIDKIFIPV-----SGTPEYEGKHLK 663
661 TKKEIVNSLFIN 672
664 NTQADVNNLFLN 675

RESULT 7
CR8AA BACUK
ID CR8AA BACUK STANDARD; PRT; 1157 AA.
AC Q45704;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pesticidal crystal protein cry8Aa (Insecticidal delta-endotoxin
DE CryVIIIa(a)) (Crystalline entomocidal protoxin) (131 kDa crystal
DE protein).
GN Name=cry8Aa; Synonyms=cryVIIIa(a);
OS Bacillus thuringiensis subsp. kumamotoensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=132267;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=NRRL B-18746 / PS50C;
RA Payne J.M., Sick A.J., Foncarrada L.;
RT "Novel coleopteran-active Bacillus thuringiensis isolate and a novel
RT gene encoding a coleopteran-active toxin."
RL Patent number EP0498537, 12-AUG-1992.
CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U04364; AAA21117.1; -; Genomic DNA.
CC HSSP; P07130; 1DLG.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
SQ SEQUENCE 1157 AA; 131010 MW; 687B5C49DE93683B CRC64;

Query Match 21.7%; Score 773; DB 1; Length 1157;
Best Local Similarity 30.5%; Pred. No. 5.7e-47;
Matches 224; Conservative 126; Mismatches 265; Indels 120; Gaps 31;

QY 6 SYQNTNEYILDGSPNN--TNMSNRYPPAKDNPFPINLDACQGRPWQD-----TWESVS 58
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Db 2 SPNNQNEYIIDATPSTSVSSDSNRYPFANEPT-----DALQNNYKDYLMKSGGENPE 55
Qy 59 DIVTIGYLYLFLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAALSI 102
Db 56 LFGNPETFISSSTTQGTIGIVGRIGALGVFPASQIASFYFVQGLWPSKSVDIWGEIM 115
Qy 103 CDLVSIIRKEVDESVDGVDAGFEGEMTAYQDYLYLHVEDLWTKSNPKLADVVVKQFOA 162
Db 116 ERVEELVDQIEKVYKDKALAEKGLGNAL-DVYQOSLEDWLENRDARTSVSNQPIA 174
Qy 163 REEDFTKLLAGLSRQKAEIILLPTTYQAAVNHLLLRDAVKYKKEGLVCPPIYPGSGR 222
Db 175 LDNLNFSSIP-SPAVSGHEVLLAVYAQAVNLHLLLRDASIFGEBWGT-----PGEIS 228
Qy 223 TDCNERLKAKIKETNYCVGHYKGLDIOIRAGTSAEVSWKFNKFRREMTLAVLDITAI 282
Db 229 RFYNRQVL-TAEYSYDCVWKYKGLDKL-GTTSKSWLNHYHOFREMTLLVLDLVALF 285
Qy 283 PTYDFEYKPLATSVELTREIYTDVGVY-----SGNGYQWERF--FSFNSVEANGTRGPGL 335
Db 286 PNVDTHYPIETTAQLTRDVTYDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVPPIHL 345
Qy 336 VTWLQAIIDYSHSINLQ-----GYLSGMGG-TRHYEDEFKNGAFQRMSTGTTNNPRNIIF 391
Db 346 FDLSSVEINTSRGGITLNDAYINYSGHTLYKRRRTADSTVYTYTANYGRITSEKNSPAL 405
Qy 392 GNTDIFKILS-----LARYAMPFGVYSIPR--HLVSRAEFPPTTLNFTLFEVNSS---G 441
Db 406 EDRDIFINSTVANLANYQK---AYGVPGSWFMVNRG---TSSTAYLYSKTHLTALQG 459
Qy 442 YSOTIESVLPKINLPPSRT-----NYSHRLSNAACVQNETSRVN-----VFGWT 487
Db 460 CTQVYES-----SDEILDRTPVAESYSHRLSH---ITSFSKNGSAYVSGPVPVMT 511
Qy 488 HTSMKKNRIYDPKITQIPAVKAFALPAGTCYAGGYTAGPGYTGDDV--TLPYQASLK 545
Db 512 HTSADLNTIYSDKITQIPAVKGMWL-----YLGSSVVGPGFTGGDILKTNPSILGTF 566
Qy 546 IRLTSAPTKNRYRLRYASGGPGPFRVERNSPSSVSNANFSRATGG-----YSSFDVVD 601
Db 567 AVTVNGSILSORYRIRYAS--TTDFEFTLYGDTIEKNRKNKTMONGASLTYYETFKPAS 624
Qy 602 TLVT-TNQSGVEIILQ-----LSGHLIVDKVERIPIDIOIEKTKCOFEGDICEGVO 657
Db 625 FITDFQRETQDKILLSNGDFSSGOEYVIDRIEFIPVDY-----EAEQ 669
Qy 658 SLETKKEIVNSLFIN 672
Db 670 DLEAAKAVNALFTN 684

RESULT 8

CR1BB BACTU STANDARD; PRT; 1229 AA.
AC Q45735; 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 13-SEP-2005 (Rel. 46, Last annotation update)
DE Pesticidal crystal protein cryIbB (Insecticidal delta-endotoxin
DE CryIb(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIbB; Synonyms=cryE15, cryIb(b);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=NRRL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects."
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut

CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; L32020; AAA22344.1; -; Genomic_DNA.
DR HSSP; P02965; IC1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1229 AA; 139771 MW; AAC949DB675C3269 CRC64;

Query Match 21.7%; Score 772.5; DB 1; Length 1229;

Best Local Similarity 32.1%; Pred. No. 6.7e-47;
Matches 229; Conservative 126; Mismatches 246; Indels 113; Gaps 30;

Qy 11 NEYEILD--GSPNNNTMSNRYPPFAKDPNIFPI-----NLDACQCRPWQDTWESYSDIV 61
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCAEVNNID-----PFVSA-STVQTGI 60
Qy 62 TIGTYLQFLLEPGIGPIVIFS-IINKLIPSSGQSAALSICDLVSIIRKEVDESVDLS 120
Db 61 NIAGRIILGVLPAPQGLASFVFLVGLWP-SGRDPWEIFLEHVEQLIRQVVTNRT 119
Qy 121 GVAFEGEMTAYQDYLYLHVEDLWTKSNPKLADVVVKQFOAREEDFTKLLAGLSR-OK 179
Db 120 AIARLEGIGRGYSYQ-QALETWLDNRNDRSRIILERYVALELDITTAI--PLFRIN 176
Qy 180 AEIILLPTVQAANVHLLLRDAVKYKKEGLVCPPLYPGSGRTDCNERLKAKIK--EY 236
Db 177 EEVPLMVAQAANLHLLLRDASLFGSEWG-----ASSDVNYQYQIRYEEY 227
Qy 237 TNYCVGWTKGLDQIRQAGTSAEVMSKFNKFRREMTLAVLDITAIPTTYDFEYKPLATSV 296
Db 228 SNHCQVWNTGLNNLR--GTNAESMLRYNQPRDLTLGLVLDLVALFSPYDTRTYPINTSA 285
Qy 297 ELTREIYTDVPGYSGNGYV--ERFF-----SFNSVEANGTRGPGLVTLWQAIIDYSHSI 349
Db 286 QLTREIYTDPIGRTNAPSFGFASTNWNFNNAFSAIEAIFRPPLHLLDFPEQLTYIAS- 344
Qy 350 NLQLGLSGMGTRHVEDFTKNGAFORMSGT-----TSNNPRNIFGNNTDIFK 398
Db 345 -----SRWSTQHMNTVWGHRLNFRPIGGTLNTSTQGLTNNTSINPTLQFTSRDVT 397
Qy 399 IISLARYAMPFGVYSIIRHLVSRAEF-FPTTLNTFLYEVNSGSGYQTIESVLPGI--- 453
Db 398 TESNA-----GTNILFTTPVNGVPWAFNFINQN--IYERGATTYSQPVGV--GLQLFD 449
Qy 454 -NKDLPPSRT-----NYSHRLSNAACVQNETSRVNFGWTHSTKMKONRIYDPDKITQIP 506
Db 450 SETELPPETTERPNYESYSHRLSLGLIIGNTLRAPVYSWTHRSADRNTTIGPNRITQIP 509
Qy 507 AVKAPALPAGTCYAGGYTAGPGYTGDDVVTLPYQASL-KIRLT-SAPTKNRYRLRYA 564
Db 510 LVKALNL-----HSGVTVVGGPGFTGGDILRNTGTGPDGIRLNINPLVSQRVYRIRA 564
Qy 565 SGCGPFRFRVERMSPPSSVSNANFSRATGG-----YSSFDYVDVTLVTTFN---QSGVEIIL 616
Db 565 STTDLQF-FTRINGITVAIGNFSRTNRGDNLEYSFRTAG-PSSTFNFNLAQSTFLGA 622

[illegible]

```
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match      21.3%; Score 756.5; DB 1; Length 719;
Best Local Similarity 31.9%; Pred. No. 4.6e-46;
Matches 224; Conservative 118; Mismatches 233; Indels 121; Gaps 32;

Qy 2 KNMSYQNTNEYILDGS-----PNNNM-----SNRYPPFAKDPNIPFINLDACQGRPWQD 52
Dy |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
4 KNQMYRSFSSNATVDSKFTDPLEHTNMELQNSHEDCLK-----MS 46
Qy 53 TWESVSDIVTGYLIQLELPGIG-----GIPV-----IFS-IINKLIPSSQS 96
Dy |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
47 EYESVEPVSVST-----IQTGIGIAGKILGNLGVPPAGVASLYSFLGELWP-KGKS 99
Qy 97 VAALSICDLVIRKEVDESVLSDGVADPEGEMTAYQDYLYLHLEDMWLTDKSNPKKLADV 156
Dy |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
100 QWEIFMEHVEELINOKISTYARNKALADLKLGLDGLAVYH-ESLESWIENRNNTKRVSV 158
Qy 157 VKQFAEEDFTKLGLSLSQKAEILLPTVQAAVHLLLRDAVKYKKEWGLVCPPL 216
Dy |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
159 KNQYIALELMFVQKLP-SFVSGSEVPLPIYAQAAVHLLLRDASIFGKEWGL----- 212
Qy 217 YPGSGRTDCNRLKAKIKETNYCVGWYKGLDQIRQAGTSAEVMSKFNKFRREMTLAVL 276
Dy |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
213 -SESEISTFYKNQSSQTSQYSDYCEWNTGLNRLR--GTNAESVMRYNQFRDRDMLV 269
Qy 277 DIIAIFPYDEKYPPLATSVELTRIHYDTPVG--YSGGNYGWERFF-----SPNSVEANG 329
Dy |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
270 DLVALFPSSYDTRMYPITPSAQLTREVTYDAIGTVHPNAPSFATTTWYNNNAPSPFTIEAAV 329
Qy 330 TRGGLVTLQADIIY----SHSINQLGLVSGWGTRHYEDFTKNGAFAQ---RMSGTTS 383
Dy |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
330 VRNPHLLDFEQVIYLSLRSWNTQ--YNNMGG--HKLEFRTGGTLNTSTQSGTWS 385
Qy 384 NNPRNIIFGNTDIFKIISLA---RYAMQPFVGYISIPRHLVSRAPF-----PPTLTNLF 434
Dy |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
386 INPVTLPSTRDVRVSTESLAGNLFITQPVNG-----VPRVDPHMKFVTHPIASDNFY 438
Qy 435 YEVSNGSYQIESVLPGLNKDLPSPRT-----NYSHRLNAAACVQNETSRVNVFGWTH 488
Dy |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
439 Y----PGVA-GIGTQLQDSENELPETTGQPNYESYSHRLSHIGLISASHKALVYSWTH 493
Qy 489 TSMKKNRIYDPKTIQIPAVKAFALPAGTGVAGGVVTVAGPVGTGGDVVTLPYQASL-KIR 547
Dy |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
494 RSADRTWINSDSITQIPLVKAFNLPASGAS-----VVRGPGFTGGDIILQRTNTGTFGDIR 548
Qy 548 LT-SAPTNNKYRVLRYASGGPGPPRVRWRSPSSVSNANFSRPAATGG-----YSSPDYVD 602
Dy |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
549 VNINPPFAQRYRLRIRYASTTNLEPHTS-INGKAINQGNFSATMWRGEDLDYKAFRTVG- 606
Qy 603 LVTFN-----QSGVEIILNLS-GYHLIVDKVEFIPIDIQIE 639
Dy |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
607 FTTTFPSFSAQSTFTIGAWNFSLGNEVDYIDRIEFVPEVTYE 648

RESULT 11
CRIBA_BACTK STANDARD; PRT; 1228 AA.
AC POA373; P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin
GN CryIIa(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
OS Name=cryIIa; Synonyms=cryA4, cryIIb(a);
OS Bacillus thuringiensis subsp. kurstaki.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=29339;
```

Db 452 TTERPNVSYSHRLSHIGIILOQSVNVVSVWTHRSADRTNTIGPNRITQIPVWKASELP 511

Qy 515 AGTGYAGYVTAGPGYTGDDVVVLPYQASL-KIRLT-SAPTNKNYRVRVLRVYASGGPGPFR 572

Db 512 QGT-----TVVRGPGTGGDILRRNTGCGFPIRVTVNGPLTKQYRIGFRYASTVDFDF 566

Qy 573 VERWSPSSVSNANFSRATG-----YSSF-----DYVDLTVTFNQSGVEIIQNLSGY-HL 624

Db 567 VSR-GGTVVNNFRFLRTMNSGDELKYNFVRRAFTTPTFTQTDIIRTSIQGLSGNGEV 625

Qy 625 IVDKVEFIPIDIOIEKTKCFEGDICKCEGVQSLETKKEIVNSLFIN 672

Db 626 YIDKIEIIPV-----TATFEAE-----YDLERAQEAVALNFTN 658

RESULT 12

Q93NM5 BACTU

ID Q93NM5 BACTU PRELIMINARY; PRT; 1228 AA.

AC Q93NM5

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cry1Ba.

GN Names=Cry1Ba;

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;

OC Bacillus cereus group.

OX NCBI_TaxID=1428;

RN NUCLEOTIDE SEQUENCE

RP Zhang J., Song F., Huang D.;

RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF368257; AAK63251.1; -, Genomic_DNA.

DR HSP; P07130; IDLC.

DR GO: 0016787; P:hydrolase activity; IEA.

DR GO: 0005102; P:receptor binding; IEA.

DR GO: 0006952; P:defense response; IEA.

DR GO: 0009405; P:pathogenesis; IEA.

DR GO: 0030435; P:sporulation; IEA.

DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin_C.

DR InterPro; IPR005639; endotoxin_N.

DR Pfam; PF03944; Endotoxin_C; 1.

DR Pfam; PF00555; Endotoxin_M; 1.

DR Pfam; PF03945; Endotoxin_N; 1.

SQ SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;

Query Match 21.2%; Score 755; DB 2; Length 1228;

Best Local Similarity 31.4%; Pred. No. 1.3e-45;

Matches 222; Conservative 120; Mismatches 264; Indels 102; Gaps 29;

Qy 11 NEVEIILGSPNNMTNMRNRYFAKDPIFIPI-----NLDACGRPWQDTWESVDIVTIGY 66

Db 7 NENEIINAVSNHQAQMDLPLDARIEDSLCTAEGNID-----PFVSA-STVQTGINIAGR 60

Qy 67 LIQFLLEPGIGGIPVIFS-IINKLIPSSGQVAALSICDLVSIIRKEVDSEVLSDGVADF 125

Db 61 ILGLVGPVPAQAGLASFVFLVGLWP-RGRDQWEIFLEHVEQLINQITENARNTALAKL 119

Qy 126 EGMTAYQDYLLHYLEDWLTDKSNPKKLADVVKQFQARBEDFTKLLAGSLRSQKAEILL 185

Db 120 QGLGDSFRAYQ-QSLEDWLENRDRDARTSRVLYTQYTALELDFLNAPLFAIRNQ-EVPLLL 177

Qy 186 PTVQANVHLLLRDAVKYKEMGLVCPPL-----YPGSGRTDCNERLKAKEYTNYCVG 242

Db 178 MVTAQAANHLHLRLDASLFGSFGTSGOIQRY-----ERQVSRTHDSDYCV 228

Qy 243 WYNGKLDQIRQAGTSAEVNSKFNKFRREMTAVLDIIAIPFTYDFEKYPLATSVELTREI 302

Db 229 WYNTGLNSLR--GTNAASWRYNQFRDLTLGLVLDLVALFPSYDTTYINTSAQLTREV 286

Qy 303 YTPDVGVSGNGYQWERFF-----SFNSVEANGTRGPGLVTVLQADIIYSHSINLQGLYLS 357

Db 287 YTDATGATGVNMAWNNVNNAPSPSAIEAAAIRSHLLDFELQLTIFGAS-----S 338

Qy 358 GMGGTRHYEDFTKNGAGAFORMSG-----TTSNNPRNIIFGNTDIFKIISLARVA 406

Db 339 RSNSTRHM-TYWRGRTIQSRPIGGGLTSTHGATNTSINPVLRFASRDVRYTESYAGVL 397

Qy 407 MQPFVGYSTPRHLVSRAEF-FPTTLNTFLYEVNNSGYSTQIESVLPGI-----NKOLPPS 460

Db 398 LMGII--YLEPFIHGVPTVFENFPQN--ISDRGTANYSQPYES--PGLQLKDSSETLPP 451

Qy 461 RT-----NYSHRLSNAACVQNETSVNVFVGWTHHTSMKKDNRIYDPDKITQIPAVKAFALP 514

Db 452 TTERPNVSYSHRLSHIGIILOQSVNVVSVWTHRSADRTNTIGPNRITQIPVWKASELP 511

Qy 515 AGTGYAGYVTAGPGYTGDDVVVLPYQASL-KIRLT-SAPTNKNYRVRVLRVYASGGPGPFR 572

Db 512 QGT-----TVVRGPGTGGDILRRNTGCGFPIRVTVNGPLTKQYRIGFRYASTVDFDF 566

Qy 573 VERWSPSSVSNANFSRATG-----YSSF-----DYVDLTVTFNQSGVEIIQNLSGY-HL 624

Db 567 VSR-GGTVVNNFRFLRTMNSGDELKYNFVRRAFTTPTFTQTDIIRTSIQGLSGNGEV 625

Qy 625 IVDKVEFIPIDIOIEKTKCFEGDICKCEGVQSLETKKEIVNSLFIN 672

Db 626 YIDKIEIIPV-----TATFEAE-----YDLERAQEAVALNFTN 658

RESULT 13

Q8KZL7 BACTG

ID Q8KZL7 BACTG PRELIMINARY; PRT; 1144 AA.

AC Q8KZL7

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cry8 protein.

GN Name=Cry8;

OS Bacillus thuringiensis (subsp. galleriae).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;

OC Bacillus cereus group.

OX NCBI_TaxID=29338;

RN NUCLEOTIDE SEQUENCE

RP STRAIN=SDS-502;

RC Asano S., Yamashita C., Iizuka T., Takeuchi K., Yamanaka S., Cerf D., Yamamoto T.;

RA "A strain of Bacillus thuringiensis subsp. galleriae containing a novel cry8 gene highly toxic to Anomala cuprea (Coleoptera: Scarabaeidae).";

RT Biol. Control 28:191-196(2003).

RL EMBL; AB089299; BAC07226.1; -, Genomic_DNA.

DR HSP; Q06117; 1J16.

DR GO: 0016787; P:hydrolase activity; IEA.

DR GO: 0005102; P:receptor binding; IEA.

DR GO: 0006952; P:defense response; IEA.

DR GO: 0009405; P:pathogenesis; IEA.

DR GO: 0030435; P:sporulation; IEA.

DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin_C.

DR InterPro; IPR005639; endotoxin_N.

DR Pfam; PF03944; Endotoxin_C; 1.

DR Pfam; PF00555; Endotoxin_M; 1.

DR Pfam; PF03945; Endotoxin_N; 1.

SQ SEQUENCE 1144 AA; 128060 MW; 98F93070C49014AB CRC64;

Query Match 21.2%; Score 754; DB 2; Length 1144;

Best Local Similarity 32.7%; Pred. No. 1.4e-45;

Matches 242; Conservative 108; Mismatches 259; Indels 130; Gaps 32;

Qy 6 SYQNTNVEIILGSPNNMTNMRN--RYPAKO-----PNIFFINL 42

Db 2 SPNNQNEVEIILDASSGTSVDSNSVRYPLANDOTTLLQNNMYKDYLRMSGEPELFF----- 57

Qy 43 DACQGRPWQDTWESVDIVT---ICTYLIQFLLEPGIGGIPVIFS-IINKLIPSSGQVA 98

Db 58 ---GNP---ETFISSSTVQTGIGVGVQVGLGALGVPFAGQIASFYFIVQGLWPSVTSVM 111
Qy 99 ALSTCDLVSITRKEVDESVLSDGVADFGEMTAVQDYLYLHLEWLTDKSNPKKLADVVK 158
Db 112 EMINKQVEDLIDQKITDSVRKLTALAGLQ--LGDGLDVYQKSLKWLNRNDTRARSVVVT 170
Qy 159 QFOAREDF--TKLAGSLSRKAEITLLPTVQAAHVHLLLRDAVKYKKEWGLVCPPLY 217
Db 171 QYIALLEDFVAKISFALSGO--EVLUSVVAQAANLHLLLRDASIFGAEWGFT----- 223
Qy 218 PGSGRTDCNERLAKIKETNTYCVGWKNGLDQIRAGTSAEVWSKFNKFRREMTLAVLD 277
Db 224 PGEIST--FYDQVTFETAQSYCYKVMYNTGLDKL--GTNAASWLKYHQFREMTEMLVLD 280
Qy 278 IIAIPPTVDFEPIKATSVLREITREYTPVGY-----SGG---NYGWERFFFSNSVEANGT 330
Db 281 LVALLFPNYDTRTYPIETTAQLTREYVTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVI 340
Qy 331 RGPGLVTLWLAIDYSHSINILQ---YLSGWGTRHYEDFTKNGAFQRMST--TSNRP 386
Db 341 RSPHLFDILSIEFYTTAGLPLANNTEYLEYVWGHSIKYKNTNASSALLERNYGTITSNKI 400
Qy 387 RNIIFGNITDIKITS---LARYAMQPFVGYSIPLRLVSRAEFFPTTLNTFLYVNSGY 442
Db 401 KYIDLANKDIFQVRLSGDLANYAQV---YGVF-----YASFTLLDKNTSGSGVGGTY 452
Qy 443 SQ-----TIESVLPGINKOLPPGRTNYSRLSNAACV---QNETS-----RV 481
Db 453 SKPHTTMQVCQNTYNTIDEIPP---ENEPLSR--GYSHLSHITSYFSKNASSPARYGNL 508
Qy 482 NVFGWTHSMKDNRIYDPKTIQIPAVKAFALPAGTGYAGGVYTAGPGYTGDDVVTLFYQ 541
Db 509 PVFANTHSADVNTVYSKDIQIPVKAHTLVSGT-----TVIKGPGFTGKNILKRTSS 563
Qy 542 ASLKIRLTS---APTWNVRLRYASGGPGPRVERWSPSSVSNANFSRATGG---YS 595
Db 564 GPLATYSVSVKSPUSQPSQRRIRYRATNTNRLFV--TISGTRYISNVNKNMKGDDLTFN 622
Qy 596 SFDYVDTLVTFNOSGVBIII-----QNLGSHLIVDKVEFIPIDIOIEKCTKCFEGDI 650
Db 623 TFD--LATIGTATFTSNYSDSLTVGADSPASGGEVVDKFLIPVN-----ATFEAE- 672
Qy 651 CRCEGVQSLTKKEIVNSL 669
Db 673 -----EDLVAKKAVKNL 685

RESULT 14

CRIBA BACTE STANDARD; PRT; 1228 AA.
ID POA374; P05517; Q45731;
AC 01-NOV-1988 (Rel. 09, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Peptidicidal crystal protein cryiBa (insecticidal delta-endotoxin
CryiB(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryiBa; Synonyms=cryA4, cryiB(a);
OS Bacillus thuringiensis subsp. entomocidus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1436;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects (By similarity).
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus (By similarity).
CC -!- SIMILARITY: Belongs to the delta endotoxin family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; X95704; CAA65003.1; -, Genomic_DNA.

DR HSP; P07130; 1DLC.

DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin_C.

DR InterPro; IPR005639; endotoxin_N.

DR Pfam; PF03944; Endotoxin_C; 1.

DR Pfam; PF00555; Endotoxin_M; 1.

DR Pfam; PF03945; Endotoxin_N; 1.

DR Sporulation; Toxin.

QY SEQUENCE 1228 AA; 139622 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match

Best Local Similarity 21.2%; Score 754; DB 1; Length 1228;

Matches 222; Conservative 121; Mismatches 263; Indels 102; Gaps 29;

Qy 11 NEYEILDGSPNNTNMSNRYPPAKDPNIPPI-----NLDACQGRPWQDTWESVDIVTIGY 66
Db 7 NENEIINAVSNHSAQMDLLPDARIEDSLCIABGNMID-----PFVSA-STVQTGINIAGR 60
Qy 67 LIQFLLEPGIGGIPVIFS-IINKLIPSSGQSVAALISCDLVSIIIRKEVDESVLSDGVADF 125
Db 61 ILGLVGFPAQGLASFYSLVGLWLP-RGRDQWEIFLEHVEQLINQOITENARNTALARL 119
Qy 126 EGETAYQDYLYLHLEWLTDKSNPKKLADVVKQFOAREDEFTKLAGSLSRKAEIILL 185
Db 120 QGLGDSFRAYQ-QSLEDWLENRDDARTSVLHTQVIALELDFLNAFLAIRNQ-EVPLL 177
Qy 186 PTYQAAVNHLLLDVAVKYEKWLVCPLP---YPGSGRTDCNERLAKIKETNTYCVG 242
Db 178 MYVQAANLHLLLRDASLFGSEFGLTSQEIQRYV-----ERQVTRDYSYCVF 228
Qy 243 WYNGKLDQIRQAGTSAEVWSKFNKFRREMTLAVLDIILFPYDPEKYPLATSVELTREI 302
Db 229 WYNTGLNLR--GTNAASWVRYNQFRDLTLGLDLVALFPYDTRTYPIINTSAQLTREV 286
Qy 303 YTDPVYSGNNGWERFF-----SPNSVEANGTRGPGLVTLWLAIDYSHSINILQGLYS 357
Db 287 YTDATGATGVNMAWNNWNNNAPSFAEAAAIRSPHLDFLEQLTIFAS-----S 338
Qy 358 GWGGRHYEDFTKNGAFQRMSTG-----TTSNPNRIIFGNTDIFKIISLARYA 406
Db 339 RWSNTRHM-TYWRGHTIOSRPIGGGLNTSTHCAATNTSINPVLRFASRDVRYTESYAGVL 397
Qy 407 MQPFVGYSIPLRLVSRAEF-PPTTLNTFLYEVNSSGYSTIESVLPGI-----NKDLPPS 460
Db 398 LWGI--YLEPIHGVPTRVFNFTNPQN--ISDRGTANYSQPYES--PGLQKDSLETLPPE 451
Qy 461 RT-----NYSHLSNAACVQNETSRVNVFGHTTSMKKDNRIYDPKTIQIPAVKAFALP 514
Db 452 TTERPNYESYSHLSHIGIILQSRVNVVYVSWTHRSADRTNTIGPNRIIOPMVKASELP 511
Qy 515 AGTGAGGVVTAAGPGYTGDDVVTLFPYQASL-KIRLT-SAPTNNKVNVRVRLRYASGGPGPR 572
Db 512 QGT-----TVVRGPGFTGDDIILRNTNTGCGFPIRVTVNGPLTQRYIGFRYASTVDFDF 566
Qy 573 VERWSPSSVSNANFSRATGG-----YSSF---DYVDTLVTFNOSGVBIIIQNLGSGV-HL 624
Db 567 VSR-GGTTVNNFRFLRTNWSGDELKYGNEVRAFTPTFTTQIQDIIIRTSIQGLSGNGEV 625
Qy 625 IVDKVEFTPIDIQIEKCTKCFEGDLCRCGVQSLTKKEIVNSLFIN 672
Db 626 YIDKIEIIPV-----TATFEAE-----YDLERAQAEVNAALFTN 658

RESULT 15

Q93T75_BACTE

ID Q93T75_BACTE PRELIMINARY; PRT; 1228 AA.

	Q93775;	
AC	01-DEC-2001 (TrEMBLrel_19, Created)	
DT	01-DEC-2001 (TrEMBLrel_19, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel_26, Last annotation update)	
DE	Delta-endotoxin CryIba2.	
GN	Name=cryIIa2;	
OS	Bacillus thuringiensis (subsp. entomocidus).	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;	
CC	Bacillus cereus group.	
OX	NCBI TaxID=1436;	
RN	[1] _SEQUENCE	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=HD-9;	
RA	Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;	
RL	Submitted (MAR-2001) to the EMBL/GenBank/DDJB databases.	
DR	EMBL; AF63025; AAKS1084.1; - ; Genomic_DNA.	
DR	HSSP; P07130; 1DLC.	
DR	GO; GO:0016787; F:hydrolase activity; IEA.	
DR	GO; GO:0005108; F:receptor binding; IEA.	
DR	GO; GO:0006952; P:defense response; IEA.	
DR	GO; GO:0009405; P:pathogenesis; IEA.	
DR	GO; GO:0030435; P:sporulation; IEA.	
DR	InterPro; IPR001178; Endotoxin.	
DR	InterPro; IPR005638; endotoxin_C.	
DR	InterPro; IPR005639; endotoxin_N.	
DR	Pfam; PF03944; Endotoxin C; 1.	
DR	Pfam; PF00555; Endotoxin M; 1.	
DR	Pfam; PF03945; Endotoxin N; 1.	
SQ	SEQUENCE 1228 AA; 139620 MW; 3DAZAA4BFS9C95C3 CRC64; Query Match 21.2%; Score 754; DB 2; Length 1228; Best Local Similarity 31.4%; Pred. No. 1.5e-45; Matches 222; Conservative 121; Mismatches 263; Indels 102; Gaps 29 Yy 11 NEYEILDGSPNTNMNSRYPPAFKDNIPFI-----NLDAQCRPWQDWESVSDIVTIGTY 66 Db 7 NENEILINAVSHSAQMQLLPDARIEDSLCIAEGNNID----PFVSA-STVGQTGINAGR 60 Yy 67 LIQFLLERPGIGIPVIFS-IINKLPSGSQAALSICDLVSIRKEVDSEVLSDGVADF 125 Db 61 ILGLVGPFAQLASFYLVELWP-RGRDWEIFLEHVEGIHQITENARNATALR 119 Yy 126 EGEMTAQDYLYHLLEDWLTOKSNPKKLADVVKFOAREEDETFLAGLSLRKAELILL 185 Db 120 QGLGDSPRAYO-QSLEDWLNRDDARTSVLHTQVTALELDPLNAMPLPAIRNQ-EVPLL 177 Yy 186 PTYYQAANVHLLLRLADAVKYKEWGLVCPEPL---YPGSRPTCNRELKKAIKEYTNYCUG 242 Db 178 MYAQAAANLHLLLRDSALFGSEFGLTSIQRIQYYY-----BRQVERTDISDYCYCE 228 Yy 243 WYNKGLOIROAGTSAEVSKFNKRREMTLAVIDIAFPFYDEKPYLATSVELTREI 302 Db 229 WINTGLNSLR--GTNAASGWRTYNQRDDLTLGLDLVALFPSYTTRTPINTSAOLTVREV 286 Yy 303 YTDPVGYSGNGYWGERFF-----SFNSVANCTRGPLWTWLOQADIYSHSNLQLGYLS 357 Db 287 YTDAIGATGVMAAMNWYNNAPSPAIEAAAIRSPHLLDFLEQLTFISAS-----S 338 Yy 358 GWGGTRHYEDTKNGAFQRMMSG-----TTSENPNRNIIFGNTDIFIKIILARYA 406 Db 339 RWSNTRHM-TYWRGHITIQSRRPIGGGLNSTHGATNTSINPVTLFPAARDVVYRTESVAGVL 397 Yy 407 MQPFVGYSI PRHLYSRAEF-PFTILTNTFLXYENVSSGYSQTIETSVLPGI-----NKDLLPS 460 Db 398 LWGI--YLEPIHGVPTVRFTNPQN--ISORGTANYSPQYES--PGLQLKDSETTELPPE 451 Yy 461 RT-----NYSHRLSNAAACVNQETS RVNVFWGTHHTSMKKDNRIYPDKITQPAPKAFALP 514 Db 452 TTERPNYESYHRLSHIGILIQRSRVVPVYSWTHRSADRNTWINGPNRITOIMPWKASELP 511 Yy 515 AGTGAYGYTAGYGTCGDVVTL PYQASL-KIRLT-SAPTWNKVVRVRLRYASGGGPPPR 572 Db 512 QGT-----TVVRGCGCTGDI LRRTNTGTCGFGR IVTVANGPLTORVRI GRFYASTVDPDF 566	

Qy	573	VERNSPSPSVSNANFSRPAATG-----YSSF-----DYVDTLVTFTNQSGVEIIIONLSGY-HL	624
Dd	567	VSR--GGTIVNFRFLRTWNSGDELUKYGNFVRRAFTPTFTQIQDIIRTSIOGLSGNGEV	625
Qy	625	IVDVKEIPIDIIQIEKTKCFEGDICRCGEVQSLETKKKIIVNSLFIN	672
Dd	626	YIDKIEIIPV-----TATFEAE-----YDLERACEAVNALFTN	658

Search completed: December 15, 2005, 10:18:39
Job time : 239 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	801.5	22.5	1156	2	S19306	parasporal crystal	
2	756	21.3	1228	2	S00873	parasporal crystal	
3	752.5	21.2	1160	2	I40589	parasporal crystal	
4	716	20.1	719	2	I39815	insecticidal prote	
5	713	20.1	719	2	I39814	insecticidal prote	
6	713	20.1	719	2	S25383	parasporal crystal	
7	710.5	20.0	719	2	I40590	cryV465 protein -	
8	682.5	19.2	1138	2	A48944	parasporal crystal	
9	680	19.1	652	2	I39811	parasporal crystal	
10	664.5	18.7	659	2	S10228	parasporal crystal	
11	664	18.7	934	2	B28838	parasporal crystal	
12	661	18.6	649	1	JH0261	parasporal crystal	
13	647	18.2	1157	1	S49247	parasporal crystal	
14	644	18.1	1174	2	S23649	parasporal crystal	
15	636	17.9	1180	2	A26858	parasporal crystal	
16	635	17.9	1180	2	I39870	parasporal crystal	
17	629.5	17.7	1154	2	S39536	parasporal crystal	
18	625.5	17.6	1176	2	A48970	parasporal crystal	
19	625	17.6	1177	2	A49785	parasporal crystal	
20	623.5	17.5	1178	1	USBSXH	parasporal crystal	
21	620.5	17.4	618	2	S11445	parasporal crystal	
22	620	17.4	652	2	A27323	parasporal crystal	
23	610.5	17.2	1176	2	JC0219	parasporal crystal	
24	606.5	17.1	1176	2	JT0241	parasporal crystal	
25	605.5	17.0	1176	2	A22617	parasporal crystal	
26	604.5	17.0	934	2	S02215	parasporal crystal	
27	604.5	17.0	934	2	A32798	parasporal crystal	
28	604.5	17.0	1160	2	S32647	parasporal crystal	
29	603.5	17.0	655	2	JC7140	protoxin - Bacillu	

172 -AGSLRQKAEILLPTVQANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNRLK 230
177 NGGLARQVAQILLPSPASAFHLLLRDRTRGTWNG-----LYNATPPINTQSKLV 231
231 AKIKEYTNYCVGYNKGLDQIRQAGTSABVMSKFNKFRREMTLAVLDIAIAPPTDYDFEKY 290
232 ELIELYTDYCVHYNRGFNELRQRTSATAMLEPHRYRREMTLWLDIVASPSLLDITNY 291
291 PLATSVELTRIYTDVGY-----SCGNVWERFF---SPNSVEANGTRGPGLVTLWLQALD 343
292 PIETDFQLSRVIYTDPIGFVHRSLRGESWFSFVNANFSDLE-NAIPNRPSPWFLNNMI 350
344 IYSHSINLQGLVSG-----WGTTRHYEDFTKNGAF--QRMSGTTSNNPRNLIIFGNTDIP 397
351 ISTGSLTLPVSPSTRARVWYGSR--DRISPANSQFITEISGQHTTATQITLGRN--IF 406
398 KIISLIARYAMQPFVGYISIPRLVSRAEFPPTT---LNTFLYE--VNSSGYS---QTIES 448
407 RVDQAQNLDDTYG-----VNRAVFHDASEGSRVYEGYIRTGTIDNPRVQNTIP 459
449 VLPINKDLPPSRNTYSHRLNA-----ACVQNETSRVNVFGWTHTSMMKDNRIYDPD 500
460 YLPGENSDI-PTPEDYTHILSTINLTGGLRQVANSRRSSIVMGWTHKSLARNNTINPD 518
501 KITQIPAVKAFALPAGTYAGGYVTAGPGYTGDDVVTLPYQASLKIRLTSAPTN--KNYR 558
519 RITQIPLTKVDTRGTGVSYN-----DPGFIGGALLQRTDHGSLGVLRVQFPLHLRQQR 573
559 VLRVASGPGPFRVERMSPSSVSNANFSRPAT-----GGYSSPDYDVTLVTFNQ 609
574 IRVRYAS-----TTNRLSVNGSFGTISQVLPSTMGLGDLRGSAIREFNTSIRPTASP 629
610 SGVEIIQ-NLSGYHLIVKVEFIPIDIQIEKTKCQPEGDICRCGEVQSLETKKEIVNS 668
630 DQIRLTIEPSFIRQSVVVDRIEFIPW-----PTR-----EAKEDLEAKKAVAS 674
669 LF 670
675 LF 676

RESULT 2
S00873
parasporal crystal protein cry8a1 - Bacillus thuringiensis subsp. thuringiensis
N:Alternate names: parasporal crystal protein cry8a1
C:Species: Bacillus thuringiensis subsp. thuringiensis
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Oct-2004
C:Accession: S00873
R:Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus
A:Reference number: S00873; MUID:88203216; PMID:3362680
A:Accession: S00873
A:Molecule type: DNA
A:Residues: 1-1228 <BRI>
A:Cross-references: UNIPROT:P05517; UNIPARC:UPI0000126BDC; EMBL:X06711; NID:g40264; PIDN
C:Genetics:
A:Gene: cryA4
A:Start codon: TTG
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 21.3%; Score 756; DB 2; Length 1228;
Best Local Similarity 31.4%; Pred. No. 1e-46;
Matches 222; Conservative 121; Mismatches 263; Indels 102; Gaps 29;
11 NEYEILDGSPNNWNSRYPFAKDPNIFPI-----NLDACQGPWQWTSVSDIVTIGTY 66
7 NENEIINAVNSHSAQMDLLPDARIEDSLCIAEGNNID-----PFVSA-STVQTGINIAGR 60
67 LIQFLLRCIGGIPVIFS-IINKLIPSSQSVAAALSIDLVSIIRKEVDESVLSDGVADF 125

61 ILGLVGPVAGQASFSYFLVGLWLP-RGRDQWEIHFLEHVEQLINOQITENARNTALARL 119
126 EGETAYODYLHYLEDMLTKSNPKLADVVVKQFOAREDEFTKLLAGSLSRQKAEILL 185
120 QGLGDSFRAYQ-OSLEDWLENDRDARTSRVLTQYIALELDLFLNAPLFAIRNQ-EVPL 177
186 PTVQANVHLLLRDAVKYKKEWGLVCPPL---YPSGRTDCNRLKAKIKYNTYCVG 242
178 MYAQANLHLLLRDASLFGSEFGLTSQEIORY-----ERQVETRIYSDYCV 228
243 WYNGKLDQIRQAGTSABVMSKFNKFRREMTLAVLDIAIAPPTDYDFEKYPLATSVELTREI 302
229 WYNTGLNSLR--GTNAASWVRYNQPRDLTLGLVLDLVALFPSYDTRTPINTSAQLTREV 286
303 YTDPIVGYSGNNGWERFF-----SPNSVEANGTRGPGLVTLWLQALDIYSHSINLQGLYS 357
287 YTDAGATGATGVNMAWNNWNNNAPSFAIAEAAIRSPHLLDLFLQLTIFSAS-----S 338
358 GGGGTRHYEDFTKNGAFQFMSG-----TTSNNPRNLIIFGNTDIFKIISLARYA 406
339 RNSNTRHM-TYWRGHTIQSRPIGGGLNTSTHGAATNTSIMPVTLRFASRDVIRTESYAGVL 397
407 MQPFFVGYISIPRLVSRAEF-FPTTLNTFLYEVSNGYSQTIESTVLPFI-----NKDLPPS 460
398 LWGI--YLEPIHGVPTVRFNTPQN--ISDRGTANYSQYES--FGLQLKDSSETELPPE 451
461 RT-----NYSHRLNAACVQNETSRVNVFGWTHTSMMKDNRIYDPKIQIPAVKAFALP 514
452 TTPRPNYSYSHRLSHIGIILQSRVNVVYVSWTHRSADRTNTIGPNRITQIPMVKASELP 511
515 ACTGAGGVVYTAGPGYTGDDVVTLPYQASL-KIRLT-SAPTNNKYNVRLRYASGGPGPPR 572
512 QET-----TVRPGFTGGDILRRNTNTGFGPIRVTVNGPLTQRYGRFYASTVDPDF 566
573 VERWSPSSVSNANFSRPATGG-----YSSF---DYDVLTVTFNQSGVEIIQNLGYS-HL 624
567 VSR-GGTTVNNFRFLRTWNSGDELKYGNFVRAFTPTFTTQIQDIIRTSIQGLSGNGEV 625
625 IVDKVEFIPIDIQIEKTKCQPEGDICRCGEVQSLETKKEIVNSLFIN 672
626 YIDKIEIIPV-----TATFEAE-----YDLERAQEAVALNFTN 658

Query Match 21.2%; Score 752.5; DB 2; Length 1160;
Best Local Similarity 31.4%; Pred. No. 1.7e-46;
Matches 233; Conservative 121; Mismatches 251; Indels 137; Gaps 35;
6 STQNTNEYILDG-SPNN-TNWSNRYPPAKDPNIFPILNDACQGPWQ----- 52
2 SPNNQNEYIIDALSPTSVDNSIRYPLAND-----QTNLTQNNMYKDYLRKMTSTNAE 55
53 -----TWESVDIVTIGTYLQIFLEPGIGIPV---IFSINKLI-----PSSGQSVAA 99
56 LSRNPGTFSIAQDAVGTGIDIVSTIIS-GL-GIPVLGEVFSILGSLGLLWPSNNWQ 113

RESULT 3
I40589
parasporal crystal protein cry8a1 - Bacillus thuringiensis
N:Alternate names: parasporal crystal protein cry8a1
C:Species: Bacillus thuringiensis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Oct-2004
C:Accession: I40589
R:Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kajii, Y.; Suzuki, N.; Hori, H.; Asano,
Curr. Microbiol. 28, 15-19, 1994
A:Title: Cloning, heterologous expression, and localization of a novel crystal protein gene
A:Reference number: I40589; MUID:94100786; PMID:7764305
A:Accession: I40589
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1160 <RES>
A:Cross-references: UNIPROT:Q45706; UNIPARC:UPI0000126CPE; EMBL:U04366; NID:g532523; PIR
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin


```

Qy 1 MKNMNSYQNTNEYEYELDGSPPNNTNMSRYPFAKDPNIPFINLDACQGRPWQDTWESVSDI 60
Db 3 LKNQDKHOSFSSNAKV--KISTDSLKNE-----TDIELQNIHEDCLK---MSEYENVEFP 54

Qy 61 VTIGTYLIQFLLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAALSICD 104
Db 55 VSAST-----IQTGIGAGKILGTGVFFAGQVASLYSFLIGELWP-KGKNQWEIFMEH 107

Qy 105 LVSIIIRKEVDSVLSDGVADPEG---EMTAYQDYLYLHLEDWLTDKSNPKKLADVVVKQFO 161
Db 108 VEEIINQKISTYARNKALTDLKGLDALAVYHD---SLESWVGNNRNTARSVVKSQYI 163

Qy 162 AREEDFTKLLAGSLRQKAEILLPTTYQAAVHLLLRDAVKYKKEWGLVCPPLYPGSG 221
Db 164 ALELMFVQKLP-SFAVSGEEVPLLPYQAANLHLLLRDASIFGKEWGLSSEI----- 217

Qy 222 RTDCNERLKAKIKEYTNYCVGWYKGLDQIROAGTSAEYVSKFNKFRREMTLAVLDIAI 281
Db 218 STFYNRQVE-RAGDYSYHCVKWSYGLNLR--GTNAESWVRYNQFRDMTLMVLDLVAL 274

Qy 282 PPTDFEYKPLATSVELTREIYTDVPG-----YSGGNYGWERFFSFSVEANGTRGPG 334
Db 275 PPSYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFTSTTWYNNAPSAIEAAVVRNPH 334

Qy 335 LVTMLOAIDY---SHSINLQGLSGWGTGTHYEDFTKNGAFO---RMSGTTNNPRN 388
Db 335 LLDFLEQVTIYSLLSRWSTNQ--YNNMWGG--HKLEFRTIGTGLNISTQGSTNTSINPVT 390

Qy 389 IIFGNTDIFPKIISLA---RYAMQPFVGYISIPHLVSRAEF-----FPTTLNTELYEVNS 439
Db 391 LPFTSRDYRTESLAGLNLFTQPVNG-----VPRVDFHWKFWTHPIASDNFYF--- 439

Qy 440 SGYSOTIESVLPKINGKDLPPSRT-----NYSHRLSNAACVQNETSRVNVFGWTHTSMMK 493
Db 494 DNRIYDPKITQIPAKAFALPAGTGAGGYVTTAGCGYTGDDVVTLTPYQASL-KIRLT-SA 551

Qy 499 TWTIEPNSITQIPLVKAFNLSSGAA-----VVRGPGFTGGDILRRNTTGTGDIRVNI 553
Db 552 PTNKYRVRRLRYASGGPGFRVERMSPSSVSNANFSRATGG-----YSSFDYVDLTVTTF 607

Qy 554 PPAQRYRVRIRYASTTDLQFHTS--INGKAINQGNFSATMNRGEDLDYKTFRTVG-FTT 611
Db 608 N-----QSGVEIIIONL-SGYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCGVQSLETK 662

Qy 663 KEIVNSLF 670
Db 657 QEKVTALF 664

RESULT 6
S25383
Parasporal crystal protein cryIIa1 - Bacillus thuringiensis
N:Alternate names: delta-endotoxin; parasporal crystal protein cryV
C:Species: Bacillus thuringiensis
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Oct-2004
R:Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
Mol. Microbiol. 6, 1211-1217, 1992
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end
A:Reference number: S25383; MUID:92269592; PMID:1588820
A:Accession: S25383
A:Molecule type: DNA
A:Residues: 1-719 <TAI>
A:Cross-references: UNIPROT:Q45752; UNIPARC:UPI000002DB73; EMBL:X62821; NID:g40289; PIDN
C:Genetics:
A:Gene: cryV
A:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin

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Query Match 20.1%; Score 713; DB 2; Length 719;
Best Local Similarity 30.2%; Pred. No. 6.3e-44;
Matches 220; Conservative 128; Mismatches 256; Indels 124; Gaps 34;

Qy 1 MKNMNSYQNTNEYEYELDGSPPNNTNMSRYPFAKDPNIPFINLDACQGRPWQDTWESVSDI 60
Db 3 LKNQDKHOSFSSNAKV--KISTDSLKNE-----TDIELQNIHEDCLK---MSEYENVEFP 54

Qy 61 VTIGTYLIQFLLEPGIG-----GIPV-----IFS-IINKLIPSSGQSVAALSICD 104
Db 55 VSAST-----IQTGIGAGKILGTGVFFAGQVASLYSFLIGELWP-KGKNQWEIFMEH 107

Qy 105 LVSIIIRKEVDSVLSDGVADPEG---EMTAYQDYLYLHLEDWLTDKSNPKKLADVVVKQFO 161
Db 108 VEEIINQKISTYARNKALTDLKGLDALAVYHD---SLESWVGNNRNTARSVVKSQYI 163

Qy 162 AREEDFTKLLAGSLRQKAEILLPTTYQAAVHLLLRDAVKYKKEWGLVCPPLYPGSG 221
Db 164 ALELMFVQKLP-SFAVSGEEVPLLPYQAANLHLLLRDASIFGKEWGLSSEI----- 217

Qy 222 RTDCNERLKAKIKEYTNYCVGWYKGLDQIROAGTSAEYVSKFNKFRREMTLAVLDIAI 281
Db 218 STFYNRQVE-RAGDYSYHCVKWSYGLNLR--GTNAESWVRYNQFRDMTLMVLDLVAL 274

Qy 282 PPTDFEYKPLATSVELTREIYTDVPG-----YSGGNYGWERFFSFSVEANGTRGPG 334
Db 275 PPSYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFTSTTWYNNAPSAIEAAVVRNPH 334

Qy 335 LVTMLOAIDY---SHSINLQGLSGWGTGTHYEDFTKNGAFO---RMSGTTNNPRN 388
Db 335 LLDFLEQVTIYSLLSRWSTNQ--YNNMWGG--HKLEFRTIGTGLNISTQGSTNTSINPVT 390

Qy 389 IIFGNTDIFPKIISLA---RYAMQPFVGYISIPHLVSRAEF-----FPTTLNTELYEVNS 439
Db 391 LPFTSRDYRTESLAGLNLFTQPVNG-----VPRVDFHWKFWTHPIASDNFYF--- 439

Qy 440 SGYSOTIESVLPKINGKDLPPSRT-----NYSHRLSNAACVQNETSRVNVFGWTHTSMMK 493
Db 440 PGYA-GIGTQLODSENEIPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADR 498

Qy 494 DNRIYDPKITQIPAKAFALPAGTGAGGYVTTAGCGYTGDDVVTLTPYQASL-KIRLT-SA 551
Db 499 TWTIEPNSITQIPLVKAFNLSSGAA-----VVRGPGFTGGDILRRNTTGTGDIRVNI 553

Qy 552 PTNKYRVRRLRYASGGPGFRVERMSPSSVSNANFSRATGG-----YSSFDYVDLTVTTF 607
Db 554 PPAQRYRVRIRYASTTDLQFHTS--INGKAINQGNFSATMNRGEDLDYKTFRTVG-FTT 611

Qy 608 N-----QSGVEIIIONL-SGYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCGVQSLETK 662
Db 612 SFLDVQSTFTIGAWNPFSSGNEVYIDRIEFPVVEVY-----EAYDPEKA 656

Qy 663 KEIVNSLF 670
Db 657 QEKVTALF 664

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RESULT 7

I40590

cryV465 protein - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Oct-2004

C:Accession: I40590

R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.

Appl. Environ. Microbiol. 61, 2402-2407, 1995

A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis

tomocidus.

A:Reference number: I39814; MUID:95314293; PMID:7793960

A:Accession: I40590

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-719 <RES>

A;Cross-references: UNIPROT:Q45709; UNIPARC:UPI000003600C; EMBL:U07642; NID:G467234; PID: C;Genetics: cryV465
A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBI:112093)
C;Superfamily: Parasporal crystal protein

Query Match 20.0%; Score 710.5; DB 2; Length 719;
Best Local Similarity 31.0%; Pred. No. 9.6e-44;
Matches 222; Conservative 120; Mismatches 244; Indels 129; Gaps 33;
QY 1 MKNMNS--YONTNEYEILDGSPNNTNMSNRYRPAKDPNIPPINLDACQGRPWQDTWESVS 58
DB 34 LKNNMEDYLRHSEHSID-----PPV-----SAS 58
QY 59 DIWT---IGTYILFLEPGIGGIPVIFS-IINKLIPSSQSVAAALSICDLVSIIRKEVD 114
DB 59 TIQTGIGAKILGTGVFPAGQIASLYSIFLGELMP-KGKSQWEIPMEHVEIINQKIL 117
QY 115 ESVLSDGVADFEGEMTAYQDYVLYHLEDMWTKDSNPKKLADVVVQFOAREEDFTKLLAGS 174
DB 118 TYARNKALSDRLGLGDALAVTH-ESLESWVENRNTRARSVVKNQYIALELMFVQKLP-S 175
QY 175 LSRQAEIILLPTVYQAAANVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCHERLKAIX 234
DB 176 FAVSGEEVPLLPYIAQAANHLHLLLRDASIFGKEWGLSASEI-----STFYNRQVE-RTR 229
QY 235 EYNTYCVGWYKGLDQIQAGTSAEWSKFNFRREMTLAVLDIIAIFPTDYDEKYPLAT 294
DB 230 DYSDDCIKWYNTGLNLR--GTNAKSWVYNGFRKDMTLWLDLVALFPFSDYTLVYPIKT 287
QY 295 SVELTREIYTPVYSGGNGY-----W--ERFFSFSNVEANGTRGPGVLTWLOAIDY-- 345
DB 288 TSQLTREYVTDAGTVHPNQAFASITWYNNAPSFSAIEAAVRSPLHLDLFEKVTIYSL 347
QY 346 -SHSINLQGLYSGWGTTHYEDFTKNGAFO---RMSGTTNNPNRIIFGNITDPIKILS 401
DB 348 LSRWSNTQ--YNNMGG--HRLSRPIGALNTSTQGSTNTSINPVTLOFTSRDVRVRES 403
QY 402 LA--RYAMQPPVGYSIPLHLYSRAEF---RPT---TLNTELYEVNSSGYSQTIESVLPG 452
DB 404 LAGLNLFLTQPVNG-----VPRVDFHWKFTPLPIASDNFYI---LGVA-GVGQLQD 451
QY 453 INKDLPPSRT-----NYSRLSNAACVQNETSRVNVFGWTHSTSMKKONRIYPKDITQIP 506
DB 452 SENELPPTTGPQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTWIEPNSITQIP 511
QY 507 AVKAFALPAGTGYAGGYTAGPGYTGDDVUTLPYQASL-KIRLT-SAPTNKNYRVLRYA 564
DB 512 LVKAFNLSSGAA-----VVRGPGFTGGDILRRNTGTGDIRVNIINPPPAQRYRRIYA 566
QY 565 SGGPGPFVRWSPSSVSNANFSRATGG-----YSSFDYVDLTVTTFNOSGVE-----III 616
DB 567 STTDLQFHTS-INGKAIQGNFSATMNRGDEDLDYKTFRTIG-FTTPFSFSDVQSTTIGA 624
QY 617 QNL-SGYHLIVDKVFIFIDIQIEKCTKQFEGDICRCEGVQSLETKKEIVNSLP 670
DB 625 WNFSSGNEVIDRIEFVPEVTY-----EAYDFEKAQEKVTLFP 664

RESULT 8
A48944
Parasporal crystal protein cry7Aa1 - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIIIC
C;Species: Bacillus thuringiensis
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: A48944
R;Lambert, B.; Hofte, H.; Annys, K.; Jansens, S.; Soetaert, P.; Peferoen, M.
Appl. Environ. Microbiol. 58, 2536-2542, 1992
A;Title: Novel Bacillus thuringiensis insecticidal crystal protein with a silent activi
A;Reference number: A48944; PMID:92384571; PMID:1514800
A;Contents: BT5137J
A;Accession: A48944
A;Status: preliminary
A;Molecule type: DNA; protein

A;Residues: 1-1138 <LAMB>
A;Cross-references: UNIPROT:Q03749; UNIPARC:UPI000002C1E6; GB:M64478; NID:G142760; PID: C;Genetics: cryV465
A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBI:112093)
C;Superfamily: Parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 19.2%; Score 682.5; DB 2; Length 1138;
Best Local Similarity 28.6%; Pred. No. 2.2e-41;
Matches 208; Conservative 128; Mismatches 262; Indels 129; Gaps 30;
QY 1 MKNMNSYONTNEYEILDGSPNNTNMSNRYRPAK--DPNIFPINLDACQGRPWQDTW--- 55
DB 3 LNNLDGYEDSN-----RTLNNSLNYPTQKALSPLSKNN-----YQDFLSITE 45
QY 56 -----SVSDIVTIGTYILFLEPGIGGIPVIP-SIINKLIPSSQSVAAALS 102
DB 46 REQPEALASNTAINTVSVTGATLSALGVPGASFITNFYLIKIALGLWPENGK-IWDEBFM 104
QY 103 CDLVSIIRKEVDSVLSDGVADPEGEMTAYQDYVLYHLEDMWTKDSNPKKLADVVVQFOA 162
DB 105 TEVEALIDQKIEEYVRNKAIAELDGLSAL-DKYQKALADWLQKQDDPEALSVATEPRI 163
QY 163 REEDFTKLLAGSLRQKAEILLPTVYQAAANVHLLLRDAVKYKKEWGLVCPPLYPGSGR 222
DB 164 IDSLF-EFSMPSPKVTGYEIPLLTVYQAANHLHLLLRDSTLYGDKWG-----FTQNNI 216
QY 223 TDCNERLKAKIKETNYCVGWYKGLDQIQAGTSAEWSKFNFRREMTLAVLDIIAIF 282
DB 217 EENYNRQKRISYSDHCTKWYNSGLSRLN--GSTYEQWVINYNRFRREMILMALDVAVF 274
QY 283 PTVDPEKYPLATSVELTREIYTPVYSGGNGYWERFFSFSNVEANGTRGPGVLTWLOAI 342
DB 275 PHDPRYSWETSQTULTREVITDPVLSISINP--DIGPFSQMENTAIRTPHLVDYDEL 332
QY 343 DIY-----SHSINLQGLYSGWGTTHYEDFTKG-----NGAFORMSGTTNNPNRN 388
DB 333 YIYTSKYKAFSHEIQDLPFWSA-----HKVSKFSQSNLYTTGIVGKTSYISSGAYS 387
QY 389 IIPGNTDIPKISLARYAMQPFVGYSIPLHLYSRAEFPPTLTNTFLYEVNSSGYSQTIES 448
DB 388 --FHGNDIYRTLAAPSVMVVPYT---QNYGVGEVFEY--GVKGHVYRGDNKYDLYTDS 439
QY 449 V--LPGINKDLPPSRTNYSRLSNAACVQNET-----SRVNVFGWTHSTSMKKONRIYPKD 501
DB 440 IDQLP---PDGEPIHEKYTHRLCHATAIFKSTPDYDNATIPISFWTHSAEYRNIYPNK 496
QY 502 ITQIPAVKAFALPAGTGYAGGYTAGPGYTGDDVUTLPYQASLKIRLTSAPTKNYR 558
DB 497 ITKIPAVKMYKLDPS-----TVVKGPGFTGGDLVKGSGTGYIGDIKATVNS-PLSQYR 550
QY 559 VRLRYASGGPGPPRV-----ERWSPSSVSNANFSRATGGYSSFDYVDLTVT-TFNQ 609
DB 551 VAVRYATNVSQGFNVYINDKITLQTKFQNTVETIGEGKDLT--YGSFGYIEYSTTIQFPD 608
QY 610 SGVEII-----TONLSYHLIVDKVFIFIDIQ-IEKCTKQFEGDICRCEGVQSLETKK 663
DB 609 EHPKTLHLSDLSNNSFFY--VDSIEFIPVDVNYAEK-----EKLSKAQ 650
QY 664 EIVNSLP 670
DB 651 KAVNTLP 657

RESULT 9
I39811
Parasporal crystal protein cry3Bb1 - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIIIB2
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
C;Accession: I39811
R;Donovan, W.P.; Rupa, M.J.; Slaney, A.C.; Malvar, T.; Gawron-Burke, M.C.; Johnson, T.
Appl. Environ. Microbiol. 58, 3921-3927, 1992
A;Title: Characterization of two genes encoding Bacillus thuringiensis insecticidal cry

A:Reference number: I39811; MUID:93119147; PMID:1476436
A:Accession: I39811
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-652 <RES>
A:Cross-references: UNIPROT:Q06117; UNIPARC:UPI0000126C14; GB:M89794; NID:gi42729; PIDN:
C:Genetics:
A:Gene: cryIIIB2
C:Superfamily: Parasporal crystal protein

```
Query Match      19.1%; Score 680; DB 2; Length 652;
Best Local Similarity 29.5%; Pred. No. 1.4e-41;
Matches 209; Conservative 125; Mismatches 233; Indels 142; Gaps 33;

QY 9 NTNEYIILDGSPNN---TNMSNRYPAKDPNIPFNLACQG-RPWQDTW-----ESVS 58
DB 5 NRSEHDTIKVTNSELQTN-HNQYPLADNPSTLEELNYKEPLRMTEDSSTVELDNSTVK 63
QY 59 DIVTIGTYLIQFLLEPGIGGP-----VIFSINKLIPSSGQSVAAALSICDLVSIIRK 111
DB 64 DAVGTGISVVGQIL--GVVGVPFAGALTSFYQSFLNTIWPSDADPWKAF-MAQVEVLIDK 120
QY 112 EVDESVLSDGVADFEGETAYQDYVLYHLEDLWLTDKSNP-----KKLADVVKQFOAREED 166
DB 121 KIEEYAKSKALAELOGLQNNFED-YVNALNSW---KKTPLSLRSKRSQDRIRELFSQAES 176
QY 167 FTKLLAGSLRSQKAEIILLPTVYQAAHVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCN 226
DB 177 HFRSNMPSFAVSKEFVLPFLPTYAQAANTHLLLLKDAQVFGSEWG-----YSSSDVAEPY 230
QY 227 ERLKAKIKEYTNYCVGWYNGKLDQIRQAGTSAEWSKKNKPREMTLAVLDLIAIPPTVD 286
DB 231 HRQLKLTQYTDHCWYNNVNGLSLR--GSTYDAWVKFNRRPREMTLAVLDLIAVLPFVD 288
QY 287 FEKYPLATSVELTRIYTDVPVYSGGNYGWERFFSFNSVE-----ANGTRGPGLVLT 337
DB 289 IRLYSGVKVTELRDIFTDPI-----FSLNLTQYEGPTFLSIENSIRKPHLPD 336
QY 338 WLQAIIDYSHSINLQGY-----LSGWGTRHYEDFTKNGAFORMS-----GTTNNP-R 387
DB 337 YLQIEFHT--RLQPGYFGKDSFNWWSG--NVYETRPSIGSKTITSFPYGDKSIEPIQ 391
QY 388 NIIFGNTDIFKILSLARYAQMP-----FVGYSIPRHLVLSRAEFPPTLNTFLYEVNS-SGYSQT 436
DB 392 KLSFDGQKYRTTANTDIAAFPDGKIYFVGTVDQKNETSTQTYDSK 444
QY 437 VNSSGYSQTIIESVLPKINKDLPSPRTN-----YSHRLSNAAC--VQNETSRVNVFGWTH 488
DB 445 RN-NGHVSAQDSI-----DQLPETTDEPLEKAYSHQLNYAECFLMQDRRGHPIPTWTH 498
QY 489 TSMKKDNRIPDKITQIPAVKAFALPAGTYAGGVYTAGPGYTGDDVVTLPYQ-----ASL 544
DB 499 RSVDFNTIDAEKITQLPVKAYALSSGAS-----IIEGPGTGGNLLFLKSSNSIAK 553
QY 545 KIRLTSAPTNKRYRLRYASGGPGPFVRERMSPPSVSNANP-----SRPATGG--YSSFDYVDTLV 595
DB 554 KVTLSAALLQRYRIRYASTNLRFLVQN-----SNNDPLVIYINKTMKDDDLTYQ 607
QY 596 SFDYVDTLVTFNQSGV-----EILL--QNLSGHLIVDKVEFIPI 636
DB 608 TFD-----LATTNSNMGFGSDKNELIIGAESFVSNEKIYIDKIEFIPIVQL 652
```

RESULT 10

S10228
parasporal crystal protein cry3Ba1 - Bacillus thuringiensis (fragment)
N:Alternate names: coleopteran-active parasporal crystal protein; delta-endotoxin
C:Species: Bacillus thuringiensis
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
A:Accession: S10228
R:Sick, A.; Gaertner, F.; Wong, A.
Nucleic Acids Res. 18, 1305, 1990
A:Title: Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of Ba

A:Reference number: S10228; MUID:90206811; PMID:2320431
A:Accession: S10228
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-659 <SIC>
A:Cross-references: UNIPROT:PI7969; UNIPARC:UPI0000126C13; EMBL:X17123; NID:940258; PIDN:
C:Genetics:
A:Gene: cryIIIB
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin; toxin

```
Query Match      18.7%; Score 664.5; DB 2; Length 659;
Best Local Similarity 29.8%; Pred. No. 1.9e-40;
Matches 209; Conservative 124; Mismatches 250; Indels 119; Gaps 35;

QY 2 KMSNRYQNTNEYIILDGSPNN---TNMSNRYPAKDPN--IPFIN-----LDACQGRPW 50
DB 7 RKNWP--NNRSEYDTIKVTNSELPTN-HNQYPLADNPSTLEELNYKEFLRMTADNSTEV 64
QY 51 QTWESVSDIVTIGTYLIQFLLEPGIGGP-----VIFSINKLIPSSGQSVAAALSIC 103
DB 65 LDS-STVKDAVGTGISVVGQIL--GVVGVPFAGALTSFYQSFLNAILWPSDADPWKAF-MA 120
QY 104 DLVSIIRKEVDESVLSDGVADFEGETAYQDYVLYHLEDLWLTDKSN--PKLADVVKQFO 161
DB 121 QVEVLIDKIEYAKSKALAELOGLQNNFED-YVNALDSWKKAPVNLRRSODRIELF 179
QY 162 AREEDFTKLLAGSLRSQKAEIILLPTVYQAAHVHLLLRDAVKYKKEWGLVCPPLYPGSG 221
DB 180 SQAESHFNRNMPSPFAVSKEFVLPFLPTYAQAANTHLLLLKDAQVFGSEWG-----YSSD 233
QY 222 RPDCHERLAKIKEYTNYCVGWYNGKLDQIRQAGTSAEWSKKNKPREMTLAVLDLIAI 281
DB 234 IAEFYQRLKLTQYTDHCWYNNVNGLSLR--GSTYDAWVKFNRRPREMTLAVLDLIAV 291
QY 282 RPTDYDEKYPLATSVELTRIYTDVPVYSGG--NYGWERFFSPNSVEANGTRGPGLVTL 339
DB 292 FPFYDVRLYSGVKVTELRDIFTDPIFTLNALQYEG-----PTFSSIE-NSIRKPHLPDYL 346
QY 340 QAIDYSHSINLQGYLSG-----WGGTRHYEDFTKNGAFORMS-----GTTNNP-RN 388
DB 347 RGIEFHT--RLRPGY-SGKDSFNWWSG--NVYETRPSIGSNDTITSFPYGDKSIEPIQ 400
QY 389 IIFGNTDIPKILSLARYAQMP--FVGYSIPRHLVLSRAEFPPTLNTFLYEVNS-SGYSQT 445
DB 401 LSFQDGQKYRTTANTDIAAFPDGKIYFVGTVDQKNETSTQTYDSKRYNGYLGA 460
QY 446 IESVLPKINKDLPSPRTN-----YSHRLSNAAC--VQNETSRVNVFGWTHSMKKDNR 497
DB 461 QDSI-----DQLPETTDEPLEKAYSHQLNYAECFLMQDRRGHPIPTWTHRSVDFNTI 515
QY 498 YPDKITQIPAVKAFALPAGTYAGGVYTAGPGYTGDDVVTLPYQ-----ASLKIRLTSAPT 553
DB 516 DREKITQLPVKAYALSSGAS-----IIEGPGTGGNLLFLKSSNSIAKFKYTLNSAAL 570
QY 554 NKRYRRLRYASGGPGPFVRERMSPPSVSNANP-----SRPATGG--YSSFDYVDTLV 604
DB 571 LQRYRRLRYASTNLRFLVQN-----SNNDPLVIYINKTMNIDGDLTYQTFDF----- 619
QY 605 TTFNQSGV-----EILL--QNLSGHLIVDKVEFIPI 634
DB 620 ATSNNSNMGFGSDTNDPIIGAESFVSNEKIY--IDKIEFIPIV 658
```

RESULT 11

B29838
parasporal crystal protein - Bacillus thuringiensis subsp. israelensis (fragment)
C:Species: Bacillus thuringiensis subsp. israelensis
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004
A:Accession: B29838
R:Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Wild, M.; Walfield, A.
J. Bacteriol. 166, 801-811, 1986
A:Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticidal

A:Reference number: A94672; MUID:86223796; PMID:3011746
A:Accession: B29838
A:Molecule type: DNA
A:Residues: 1-934 <THO>
A:Cross-references: UNIPROT:P09662; UNIPARC:UPI00001781A0; GB:M12662; NID:g143228

Query Match 18.7%; Score 664; DB 2; Length 934;
Best Local Similarity 30.5%; Pred. No. 3.6e-40;
Matches 228; Conservative 96; Mismatches 273; Indels 150; Gaps 34;

```
QY 4 MNSYONTNEVEILDGSPNNTNSN---RYPPAKDPNIPFIN-----LDACQGRW--- 50
Db 1 MNPYQNKNEYIFNAPNSGFSKSNYSRYPLANKPN-QPLKNTNYKDWLNVCDOOQYGN 59
QY 51 -----QDTWESVS-DIVTIGTYILQFLLEPGIGIPVIFSII---NKLIPSSGOSVAA 99
Db 60 NAGNFASSETIVGSAGIIVGTML-----GAPAPVLAAGIISFGTLLPIFWGSDP 112
QY 100 LSIC-DLVSIIKEVDE-----SVLSDGVADPEGEMTAQDYLYLHYLEDW--LTDKSNP 150
Db 113 ANVQDOLLNIGRPQIEIDKNIINVLTSIVTPIKNLQDKYQBF--DKWEPARTHANA 168
QY 151 KKLADVQKQFQAREEDFTKLLAGLSRQKAEILLPTTYQAAHVHLLLRDAVKYKKEWG 210
Db 169 KAVHDL---FTTLEPIIDKDLMLKNNASYRIPTLPAYAQIATWHLNLLKHAATYYNIW- 224
QY 211 LVCPPLYPGSGRTD--CNERLAKIKEYTNYCVGWYKGLDQIRQAGTSAEYVWSKENKER 268
Db 225 LQNGINSTFTSNSSYYQYLKRRKIQEYDYCIQTYNAGLTWIR-TNTNA-TWNMYNTYR 282
QY 269 REMTLAVLDIIAIFPTYPEKPLATSVELTREIYDTPVGYSGNGYGERFFSFNSVEAN 328
Db 283 LEWTLVLVDLIAIFPNYDEKPIGVKSELIREVIT-----NVNSTFTITILENG 334
QY 329 GTRGPGLVTLQAIDIIYSHSINLQGLYLSGWGTRHYEDFTKGNGAF-----QRMSGTTSN 384
Db 335 LTRNPTLFTWINGRFP-----TRNSRDILDYDIFSTFGNQMAFTHTN 378
QY 385 NPNRIIFG-----NTDIFKIIISLARYAMQPFVGSIPRH-----LVSRAEFFPTTLNT 432
Db 379 DDRIIHWAGVHGNIIISQDTSKVPFP--YRNKPIDKVEIVRHREYSIDIYEMIFPSSSEV 436
QY 433 FLYEVNSSGYSTIESVLPGLNKDLPSPRT---NYSHRLSNA--CVQNETSRVN 482
Db 437 FRYSNS-----TIENNYKRTDSYMLPKQTWKNEEYGHLSYIKTDNYIFSVVRRRRV- 490
QY 483 VFGWTHSKKKNRIYDPDKITQIPAVKAFALPAGTGAGGYTAGGYTGAGDVVTLPLYQA 542
Db 491 AFSWHTTSVDFQNTIDLDNIQIHALKALKVSSDS-----KIVKPGHGTGGDLVILKDSM 545
QY 543 SLKIRLTSAPTNWTRVRLRYASGP-----GPFVRWSPSSVSNANFSRATG- 592
Db 546 DFRVFLK-NVSRQYQVIRYATNAPKTVFLTGIDTISVELPSTTSRQNP-----ATDL 600
QY 593 GYSSFDYVDLVTTFNQS--GVEIILQNLG-----YHLIVDKVEFIPIDQIEKTKCQ 645
Db 601 TYADFGYVTFPRVFNKTFEGEDTLMTLYGTPNHSYNIYIDKIEFIPITQSVLDYTE-- 658
QY 646 FEGDICRCBGVQSLETKEIVNSLFIN 672
Db 659 -----KQNIETQKIVNDLFWN 675
```

RESULT 12
JH0261
parasporal crystal protein cry3Cal - Bacillus thuringiensis subsp. kurstaki (strain B111)
N:Alternate names: parasporal crystal protein cryIIID
C:Species: Bacillus thuringiensis subsp. kurstaki
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C:Accession: JH0261; S18944
R:Lambert, B.; Theunis, W.; Aguda, R.; Van Audenhove, K.; Decock, C.; Janssens, S.; Seuri
Gene 110, 131-132, 1992
A>Title: Nucleotide sequence of gene cryIIID encoding a novel coleopteran-active crystal

A:Reference number: JH0261; MUID:92184108; PMID:1544571
A:Accession: JH0261
A:Molecule type: DNA
A:Residues: 1-649 <LAM>
A:Cross-references: UNIPROT:Q45744; UNIPARC:UPI0000126C15; EMBL:X59797; NID:g40287; PID

C:Genetics:
A:Gene: cryIIID
C:Superfamily: Parasporal crystal protein

Query Match 18.6%; Score 661; DB 1; Length 649;
Best Local Similarity 30.3%; Pred. No. 3.4e-40;
Matches 216; Conservative 108; Mismatches 234; Indels 156; Gaps 35;

```
QY 9 NTNEYILDGSPNN--TNMSNRYPPAKDPNIPFINLDCACQGRPQDWTWESV---SDIV 61
Db 5 NRSEHTIKATENNEVSNHHAQPLADTPTLEELNYKEFLRRTDNNVEALDSSTTKDAI 64
QY 62 TIGTYILQFLLEPGIGIP-----VIF--SIINKLIPSSGOSVAALSICDLVSIIRKEDV 114
Db 65 QKGISIIGDLL--GVGFPYGGALVSPYTNLLNTWIP--GEDPLKAFMQQVEALIDOKIA 120
QY 115 ESVLSGVADPEGEMTAQDYLYLHYLEDWLTDSNPKKLADVVVKQFOARE-----EDFTK 169
Db 121 DYAKDKATAELOGLKNVFKD--YVSALDSW--DKT-PLTLRDRSGRIRSELFSAESHR 176
QY 170 LLAGLSLRQKAEILLPTTYQAAHVHLLLRDAVKYKKEWGLVCPPLYPGSGRTDCNERL 229
Db 177 RMPSPFVAGYEVLFPLPTTAQAANTHLLLDKDAIYGTDWG-----YSTDDLNEFHTKQ 230
QY 230 KAKIKEYTNYCVGWYKGLDQIRQAGTSAEYVWSKFNKFRREMTLAVLDIIAIFPTYPEK 289
Db 231 KOLTIEYTHCAKWKYAGLKLK--GSTYEWKFNRYRREMTLVLDDLTLPFLYDVRT 288
QY 290 YPLATSVELTREIYDTPV-----GYSGNGYGERFFSFNSVEANGTRGGLVTLQAII 342
Db 289 YTKGVKTELTRDVLTPDIVAVNNMNGVG-----TTFSNIE-NYIRKPHLPDYLHAI 338
QY 343 DIYSHSINLQGLYLSGWGTRHYEDFTKGNGAFQRMSS-----GTTSN-NPNRI 389
Db 339 QPHS-----RLQPGYF-----GTDSP-NYWSNGYVSTRSSIGSDEIRSPFYGNKSLDQNL 390
QY 390 IFGNTDIFKIIISLARYAMQPFVGSIPRHLSRAEFPTTLNTFLYEVNSSGY----- 442
Db 391 EFNKEGVFRVANGNLAVWP-VGTG-----GTXHSGVTYQVSOYNDKRDV 437
QY 443 -SQTIES-----VLPGLNKDLPSPRTN-----YSHRLSNAAC--VQNETSRVNVFGW 486
Db 438 RTQTYDSKRNVGSI VFDSDIQ-LPPTTDBSEKAYSHQLNYYVRCFLQGGRIIPVFTW 496
QY 487 THTSMKKNRIYDPDKITQIPAVKAFALPAGTGAGGYTAGGYTGAGDVVTLPLYQASIKI 546
Db 497 THKSVDFTYNTLDSSEKITQIPFVKAFILVNST-----VWAGPGFTGGDIIKCTNGSGJTL 551
QY 547 RLTSAPT---NKNYRVLRYASGPGPFVRWSPSSVSNANFSRATGGSV-SFDYVD- 601
Db 552 YTPPADLTYSTKYKIRIYASTSQVRFGID-----LGSYTHSISIFDK 595
QY 602 -----TLV-TTFNQSGV---EIIQNL-----SGYHLIVDKVEFIPID 635
Db 596 TWDKGNTLYNSFNLSVSRPIEISGKNKIGVSGVGGIGSGDEVYIDKIEFIPMD 649
```

RESULT 13
S49247

parasporal crystal protein cry9Cal [validated] - Bacillus thuringiensis
N:Alternate names: parasporal crystal protein cryIIF
C:Species: Bacillus thuringiensis
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
C:Accession: A59350; S49247
R:Lambert, B.; Buyase, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.;
Appl. Environ. Microbiol. 62, 80-86, 1996
A>Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity aga
A:Reference number: A59350; MUID:96141404; PMID:8572715

A:Accession: A59350
A:Molecule type: DNA
A:Residues: 1-1157 <LAM>
A:Cross-references: UNIPROT:Q45733; UNIPARC:UPI000002F5A5; EMBL:Z37527; NID:G547554; PID
A:Experimental source: serovar colworthi
C:Comment: This parasporal crystal protein, active against corn borer and other insects,
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 18.2%; Score 647; DB 1; Length 1157;
Best Local Similarity 27.3%; Pred. No. 8.8e-39;
Matches 198; Conservative 127; Mismatches 287; Indels 112; Gaps 25;

```
QY 9 NNEVEILD---GSPNNINMSNPPFAKDPNIPINLDACGRPWQDTWESVSDIVTIG 64
DB 5 NQNEYIIDAHCPCGDDV--RYPLASDPNA-----ALQNNYKYLQMTDSDYT-D 55
QY 65 TYLIQFLLEPGIGIPVIFSIINKL-----IPSSGQSVAALSIC-----103
DB 56 SYINPSLSISGRDAVQTALTVVGRILGALGVFSGQIVSFYQFLNLTLPVNDTALWEAF 115
QY 104 --DLVSIIRKVESVLSGVDADFGEMTAYODYLHYLEDWLTOKSNPKKLADVVKQFQ 161
DB 116 MRQVEELVNOQITEFARNQALRQGLGDSF--NVYQRSLOQLWLANDRNDTRNLSVVRQFI 174
QY 162 ABEEDFTKLAGSLRQKAEIILLPTYQAAVNHLLLRDAVKYKKEWGLVCPPLYPGSG 221
DB 175 ALDLDFVNAIP--LFAVNGQQVPLLSVYAQAVNLHLLLLKDALSLFGEGWGT-----QGBI 228
QY 222 RTDCNERLKAKIKEYTNYCVGWYKGLDQIROAGTSAEVMSFNKFRPREMTLAVLDIAI 281
DB 229 STYIDRQLELTAK--YNYCETWYNTGLDLRL--GNTESWLRYHQFRREMTLVLVDVAL 285
QY 282 PFTYDFEKYPLATSVELTREIYDPVYSG-----GNYGWERFFSFSVEANGTRGPG 334
DB 286 PFYDVRLYPTGSNPQLTREVTDPVFNPPANVGLCRRWGTNPYNTFSELENAFIRPPH 345
QY 335 LVTWLQADIIYSHSINLQGLYSGGCTHYEDFTKNGCAFQMSGTTNNPRNIFGNT 394
DB 346 LPDRLNLSLTISSNRPFPVSNFMDYNSGHTLRSLYNDLSAVQDSYGLITTTTRATINPGVD 405
QY 395 DIFKIIISLARYAMQPFVGYSIPIRLHVSRAEFPTTLNTEFLYEVNSSGYSTIESVLPGLN 454
DB 406 GNTRIESTAVDRSALIGI-----YGVNRASFVPGGLFNGTTPANGGCRDLDT-----N 456
QY 455 KDLPPSRNTYS--HRLSNAACVQNETSR-----VNVFGWTHTSMKDNRIYDPKIT 503
DB 457 DELPDESSTGSTRHLSHTVTFPSFQINQAGSIANAGSVPTYYVTRDRVDLNNITIPNRI 516
QY 504 QIPAVKAFALPAGTGYAGGYTAGGYTGDDVTLTPYQASL--KIRLT--SAPTNKNYRVL 561
DB 517 QLPLVKASAPVSGT-----TLVKGPGFTGGILRRTNGTFTGLRVTNSPLTQQYRLRV 571
QY 562 RYASGCGPFRVERMSVSPSVSNANFSRATGG-----YSSPDYVDTLVT-----TFNQS 610
DB 572 RPASTGNFSIRVL--GGVSGIDVRLGTSWNROQLLEYSEFFTRFETFTGFPNPPFTQA 630
QY 611 GVEIILQNLGSY-----HLVVDKVEFIPIDIQIEKCTKQCEGDIQCEGVSQSLTKKEIV 666
DB 631 -QELLTVNAEGVSTGGEYIDRIEIVPVN-----PAREAEEDLEAAKAV 674
QY 667 NSLF 670
DB 675 ASLF 678
```

RESULT 14
S32649
parasporal crystal protein cryIa3 - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004
C:Accession: S32649
R.Lambert, B.

submitted to the EMBL Data Library, April 1993

A:Reference number: S32645
A:Accession: S32649
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1174 <LAM>
A:Cross-references: UNIPROT:Q45749; UNIPARC:UPI00000BF0F3; EMBL:Z22512; NID:G295865; PID
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 18.1%; Score 644; DB 2; Length 1174;
Best Local Similarity 29.2%; Pred. No. 1.5e-38;
Matches 202; Conservative 115; Mismatches 255; Indels 120; Gaps 26;

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QY 24 NMSNR---YPPAKDPNIPINLDACGRPWQDTWESVSDIVTIGTYLIQFLLEPGIGIP 80
DB 4 NQNOCVPYCNLSNPEVEILSEERSTGRPLD-----ISLSLTRFLSEFVPGVG 53
QY 81 VIFSIIINKLIPSSGOSVAALSICDLVSIIRKVESVLSGVDADFGEMTAYODYLHYL 140
DB 54 VAFGLFDLWGTITPSEWSLFLQIQEQLIEQRIETLERNRAITTLRGLADSY-EVILEAL 112
QY 141 EDWLTOKSNPKKLADVVKQFQAREEDFTKLAGSLRQKAEIILLPTYQAAVNHLLLR 200
DB 113 REWEENPNNAQLREDVRIRF--ANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLR 171
QY 201 DAVYKKEWGLVCPPLYPGSGRTDCNERLKAKIKEYTNYCVGWYKGLDQIROAGTSAEV 260
DB 172 DAVSFGQCGWGLDIATV-----NNHYNRLINLIHRYTEHCLDTYNOGLENLR--GTNTRQ 223
QY 261 WSKENKFEREMTLAVLDIAIPTDYDFEKYPLATSVELTREIYT-----DPVGYSGNY 314
DB 224 WSKFNQFRRELTVLVDIIVALFPNDYDARAYPTQTSQLTREIYTSVIEDSPVSAKIPN- 282
QY 315 GWERFFSFSVEANGTRGPGLVTLQADIIYSHSINLQGLYSGGCTHYEDFTKNGA 374
DB 283 -----GFNRAEF--GVRPPHLMDFWNSLFTAETVRSQ---TWGSG--HLVS----- 322
QY 375 FORMSGTTNNPRNI--IFGNTDIFKIIISLARYAMQPFV-----GYSIPRLHVS- 421
DB 323 ----SRNTAGNPNFPIYIGIFNPGGAIWIADEPRPFYRTLSDPVFVRGFGNPHYVGL 378
QY 422 RAEPFPTTLNTEFLYEVNSSGYSTIESVLPGLNTEFLYEVNSSGYSHLSNAACVQ----- 475
DB 379 RGVAFOQTNTNTRTFERNSTIDSLDEIIPQDMSGAP--WNDYSHVLNHWTFVVRWGEIA 436
QY 476 -NETSRVNVFGWTHTSMKDNRIYDPKITQIPAVKAFALPAGTGYAGGYTAGPYTGDD 534
DB 437 GSDSWRAPMFSTHRSADRTNINPNIIQIPAVKAHL-----HSGSTVVRGPGFTGGD 491
QY 535 VVTLPYQ---ASLKIRLTSAPTNKNYRVLRYASGCGPFRVERMSVSPSVSNANFSR- 589
DB 492 LLRRNTGTGFADIRVNIT--GPLSQRYRVRIRYASTTDLQF--FTRINGTSVNQGNFQRTMN 549
QY 590 -----ATGGVSS--FDYVDTLVTTFNQSGVEIILQNLSGYHLIVDKVEIPDIOI 638
DB 550 RGNLESNGNFRTAGSTPESFSNA-----QSTFTLTQAFSNOEYVIDRIEFVPAEVT 603
QY 639 EKCTKQCEGDIQCEGVSQSLTKKEIVNSLF 670
DB 604 EA-----ESD-----LERAQAVNALF 620
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RESULT 15
A26858

parasporal crystal protein cry4Aa1 - Bacillus thuringiensis subsp. israelensis
N:Alternate names: parasporal crystal protein cryIVA
C:Species: Bacillus thuringiensis subsp. israelensis
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 05-Oct-2004
C:Accession: A26858; S48691
R:Ward, E.S.; Ellar, D.J.
Nucleic Acids Res. 15, 7195, 1987
A:title: Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding

A:Reference number: A26858; MUID:88015571; PMID:2821500
A:Accession: A26858
A:Molecule type: DNA
A:Residues: 1-1180 <WAR>
A:Cross-references: UNIPROT:P16480; UNIPARC:UPI000016EA42; CB:Y00423; NID:940351; PIDN:C
A:Note: the authors translated the codon GCA for residue 308 as Thr
R.Nishimoto, T.; Yoshieue, H.; Ihara, K.; Sakai, H.; Komano, T.
FEBS Lett. 348, 249-254, 1994
A:Title: Functional analysis of block 5, one of the highly conserved amino acid sequence
A:Reference number: S48691; MUID:94307434; PMID:7913448
A:Accession: S48691
A:Molecule type: DNA
A:Residues: 667-676 <NIS>
A:Cross-references: UNIPARC:UPI000017819A
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 17.9%; Score 636; DB 2; Length 1180;
Best Local Similarity 29.1%; Pred. No. 5.8e-38;
Matches 219; Conservative 112; Mismatches 288; Indels 134; Gaps 34;

QY 4 MNSYQNTNEYELTLDGSPNNTNMSN---RYPFKADPN--IFPIN-----LDACQ-----GRP 49
DB 1 MNPYQNKNEYETLNASQKLNISNNTRYPIENSFKQLQSTNYKDWLNMCQONQOYGGD 60

QY 50 WQ---DTWESVSDIVTIGTYLIQFLLEPGIGGIPVIF-SIINKLIPSSGQS-VAALSICD 104
DB 61 PFTFDISGELSAYTIVGTVLGFGTPLGLALIGFTGLIPVLPPAQDSNTWSDFITQ 120

QY 105 LVSIIRKEVDESVLSDGVADFEGETAYQDYVLYHLEWLDTKSNPKKLADVVVKQFARE 164
DB 121 TKNIIKKEIASTYISNANKILNRSFNVISTYHNH-LKTW-ENNPNPQNTQDVRTQIQLVH 178

QY 165 EDFTKL---LAGSLRQKAE-----ILLPTVYQANVHLLLRDAVKYK-----KEWG 210
DB 179 YHFQNVIPELVNSCPPNPSDCDYNILVLSYQAANLHLTVLQAVKFEAYLKNNRQPD 238

QY 211 LVCPLPYGSGRTDCNERLKAKIKVTNYCVGMNKGDLDIR--QAGTSAEV-WSKENK 266
DB 239 Y-----LEPLTAIDYVPLTKAIEDYTNVCVTKYKGLNLIKTPTDSNLDGNINWNTYT 294

QY 267 PAREMTLAVLDIAIFPTVDFEYKPLATSVELTREIYTDVPGYSGNYGWERFFSFNSVE 326
DB 295 YRTKMTTAVLDVVALFPNVDGKYPVQSELTRIIY-QVLNFEESPY---KYDFQYQE 350

QY 327 ANGTGPGGLVTLQALDIYSHSINQLGYLSGWSGGRHYEDFTKNGAPQRMSTSN-N 385
DB 351 DSLTRRPHLFTWLSLNFYKQAQTTNNPF-----TSHYMF-----HYTLDNIS 395

QY 386 PRNIIFGN---TDIEKIISLAR--YAMQPFV-----GYSIPRLVSRAEFPPTTLNTPLY 435
DB 396 QKSSVFGHNHVTDKLSLGLATNIYIFLNLVSLDNKYLNDYNNISKMDFFITNGTRLLE 455

QY 436 EVNSSGYQTIESVLPFI-----NKLPPSRNTYSHRLS---NAACVQNETS 479
DB 456 KELTAGSQITVDVKNIFGLPLKARENQGNPTLPFTYDNYSHILSPKLSLSIPATYKT 515

QY 480 RVNFGWTHSMKKDNRIYDPDKITQIPAVKAPALPAGTGYAGGYTAGPGYTGDDVTLPL 539
DB 516 QVYTFAMTHSSVDPKNTIYTHLTQIPAVKANSL--GT---ASKVVQPGHGTGGDLI--D 568

QY 540 YQASLKIRLTAPTNTKYNRVLRYASGGPFR-VERWSPSSVSNANFS-RPATCG----- 593
DB 569 FKDHFKITCQHSNFOQSYFIRIYASGSANTRAVINLSIPGVAELGMALNPTFSGDTYT 628

QY 594 ---YSSFDYVD-----TLVTFNOSGVEIIQNLGSHLIVDKVERIPIDIQIE 639
DB 629 NLKYDFQYLFESNEVKFAPNQNISLVNRSDV-----YNTTVLIDKIEFLPTRSIR 682

QY 640 KCTKQPEGDICRCBGVQSLETKKIVNSLFIN 672
DB 683 EDRE-----KQKLETVOQIINTFYAN 703

Search completed: December 15, 2005, 10:19:26
Job time : 45 secs